

## SUPPLEMENTARY MATERIALS

# An Anatomic Gene Expression Atlas of the Mouse Brain

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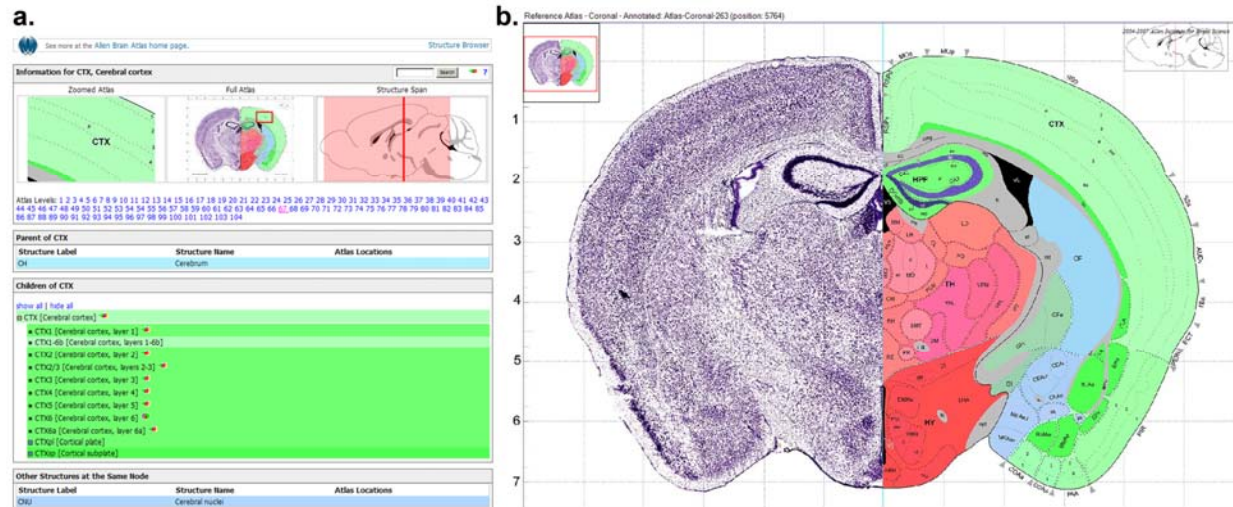
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## **A. Supplementary Methods**

**ISH processing and imaging.** ISH tissue sections (25µm thick) were generated from 56 day old male C57BL/6J mouse brains. Each section was labeled for a specific gene using a semi-automated ISH protocol<sup>1</sup>. The Image Capture System consists of 10 independent Leica DM6000B microscopes with a Leica DC500 camera, and mounted on an air table to isolate the microscope from external vibration sources. The image capture procedure is essentially fully automated and collects each tissue section at 10x magnification and 1.07 µm/pixel resolution storing directly into the JPEG2000 format. Details can be found in<sup>1</sup>.

**3D reference atlas.** The process of 3D mapping starts with atlas-based annotation using a novel high-resolution anatomic atlas, the Allen Reference Atlas (ARA). The ARA volume was derived from 528 coronal Nissl stained sections (25µm thick) from an unfixed, frozen mouse brain. From this set, 132 sections, with 100µm spacing, were annotated for over 1000 brain structures to form the ARA (**Supplementary Fig. 1**). The 3D Nissl volume is a result of a rigid reconstruction process where each section is reoriented to match the adjacent images as closely as possible, forming an assembled 3D volume. A 1.5T low resolution 3D average MRI volume was used to ensure that the reconstruction resulted in a realistic volume<sup>2</sup>. Each reoriented Nissl image was then downsampled and converted to grayscale to form an isotropic 25µm grayscale volume. Further boundaries for 208 large structures and structural groupings were extracted from the ARA and projected and smoothed onto the 3D atlas volume to provide the accompanying structural annotation in the AGEA interface (**Fig. 1b**). An additional decomposition of the cortex into an intersection of 202 regions and areas was performed.

The 3D reference atlas is divided into a 200µm<sup>3</sup> grid consisting of 67 coronal x 41 horizontal x 58 sagittal cells or voxels (sum=159,326) of which 51,533 voxels are masked to intersect the ABA data. These 200µm voxels form the smallest spatial unit for analysis.



**Supplementary Figure 1. Neuroanatomy of the Allen Reference Atlas.** (a) Web-view versions (screenshots) of the Allen Brain Atlas that are accessible through the AGEA interface, with the neuroanatomical ontology used in the Allen Reference Atlas. A direct link is available from each structure in AGEA to detailed anatomy and parent/child relationships. (b) A representative full reference atlas plate, which can be viewed in high resolution, is shown.

**Expression energy statistics.** An adaptive threshold algorithm<sup>3</sup> identifies expressing cells in each 2D tissue section, resulting in an expression mask that effectively classifies each pixel in the image as to whether that pixel represents expressing cells (**Fig. 1d**). A single statistic called *expression energy* is a convenient representation of the information content in each voxel and represents the product of expression area and expression intensity in that voxel<sup>1,3</sup>.

*Expression energy*  $E(C)$  for a cubic voxel  $C$  is defined as follows:

$$E(C) = \frac{\sum_{p \in C} M(p) \times I(p)}{|C|}$$

where  $p$  is a image pixel that intersects voxel  $C$ ,  $|C|$  is the total number of pixels that intersect  $C$ ,  $M(p)$  is the expression segmentation mask which is either 1 ("expressing" pixel) or 0 ("non expressing" pixel) and  $I(p)$  is the grayscale value of the ISH image intensity defined as  $\text{Gray} = 0.3 \times \text{Red} + 0.59 \times \text{Green} + 0.11 \times \text{Blue}$ . The advantages of defining expression energy in this way is that it can be robustly computed over all brain regions; it is easily normalized to account for different image resolution and/or section sampling frequency; it is amenable to smoothing for noise suppression; and it combines features of expression intensity and expression density into a single measurement.

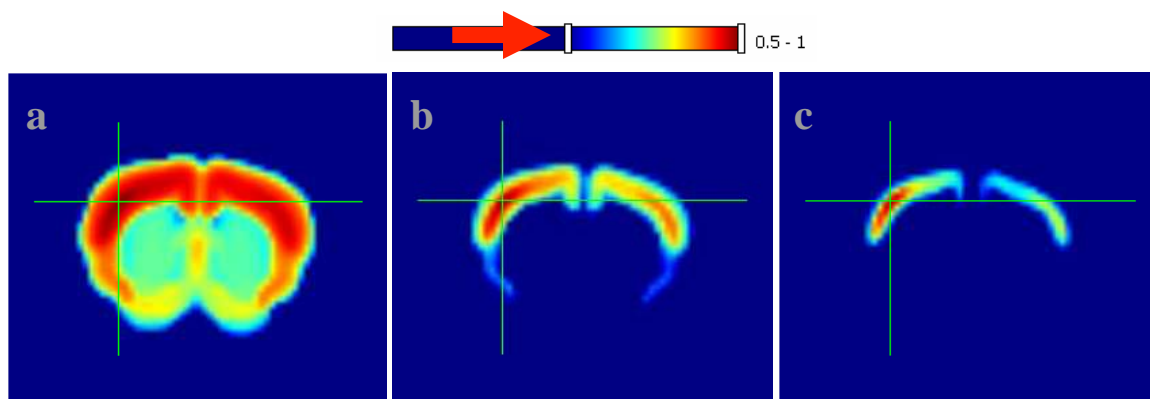
**Transcriptome profile.** For each voxel, a transcriptome profile, over a predefined set of genes, can be constructed as a vector of expression energy values where each component of the vector represents a gene in the dataset. AGEA transcriptome profiles were constructed from 4,376 coronal image series in the ABA (See **Methods: AGEA dataset**).

**AGEA Application.** The AGEA application is multi-user, has no plug-ins and uses AJAX Java server and C++ in a servlet application with Java script on the client. It is fully linked with the ARA and ontology and does slicing and threshold computation of the 3D correlation volumes at user access time. Detailed description of the user interface can be found on the accompanying online tutorial (<http://mouse.brain-map.org/pdf/AGEA.pdf>).

**AGEA Correlation maps.** Pearson correlation<sup>4</sup> was used to measure the similarity between two transcriptome profiles or vectors for each pair of distinct voxels. Correlation essentially measures linear relationship; two voxels have high positive correlation when high (or low) expression energy in one voxel is associated with high (or low) expression energy in the other voxel. A higher relative correlation value indicates greater fidelity to the linear relationship model.

To make navigation and display of this large set ( $>10^9$ ) pair-wise correlation values intuitive, we have used a reference or “seed” voxel paradigm. To use the **Correlation** map tool, a user selects the “seed voxel” by moving the red cross-hairs on the 3D Nissl atlas (**Fig. 2a, upper panels**), the corresponding 3D correlation map is then displayed (**Fig. 2b, lower panels**) as a 24-bit false color images. The color at each voxel in the correlation map represents the correlation between this voxel and the “seed voxel”. A scale bar enables users to change the dynamic range of the color map, in which hot and cool colors represent higher and lower correlation respectively. The associated numerical data can be downloaded via links below the correlation maps.

**Supplementary Figure 2** illustrates the multiple scales on which gene expression can be analyzed. In the first panel, the mass of orange/red voxels indicates the cerebral cortex as a co-expressing unit. A subtle change from dark orange and light orange reflects the demarcation between the isocortex (or neocortex) and the olfactory areas. As we decrease the mapping range to [0.85,1] (**Supplementary Fig. 2b**), the existence of a coherent laminar layer 5 becomes more apparent. By decreasing the range even further to [0.92,1] in (**Supplementary Fig. 2c**), a more local region in the somatosensory cortex emerges.



**Supplementary Figure 2. Changing correlation dynamic range.** The effect of changing the threshold color scale bar for a voxel seed in Layer 5 of the cortex. Contracting toward a more restricted dynamic range focuses the spatial relationship first on the cortex-wide scale and then subsequently on a more regional intra-layer 5 scale. Thresholds are [0.5,1], [0.85,1], and [0.92,1] for a, b, and c respectively.

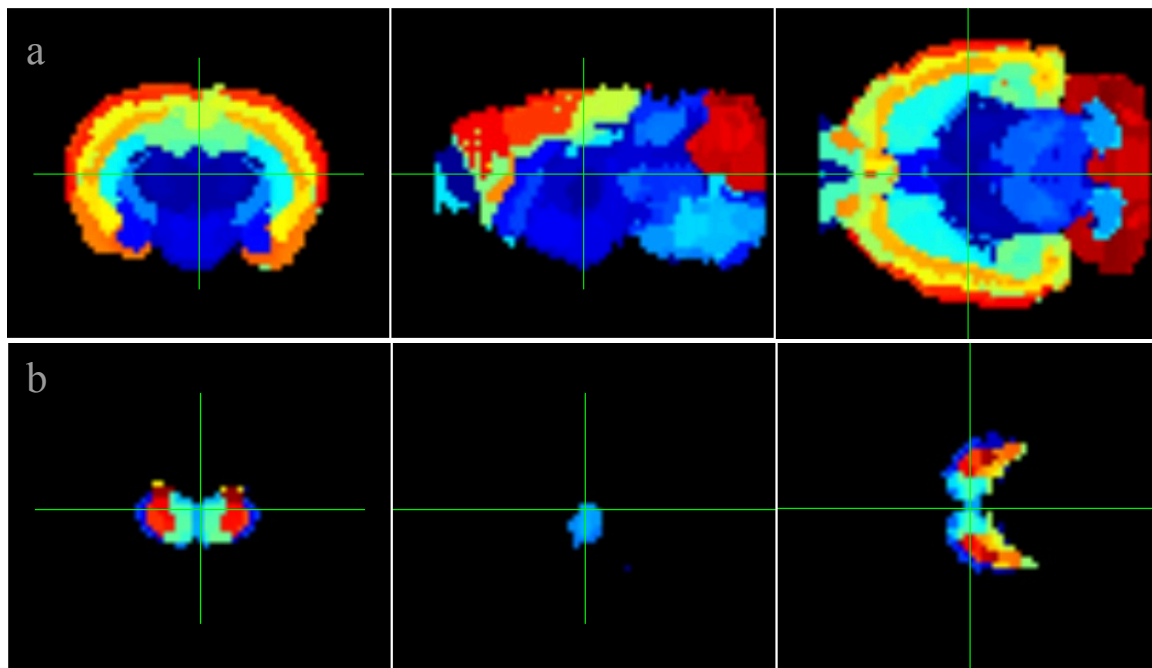
**AGEA Clusters.** This tool represents a purely transcriptome derived hierarchical spatial organization of the adult mouse brain. The 51,533 AGEA correlation maps were used to create hierarchical grouping or clustering of voxels with similar composite gene expression profiles across the AGEA dataset. The

spectrum of gene expression patterns in the brain is complex displaying both intra-structure widespread expression and multifarious regional specificity. We have used a simple strategy that captures the various scales of spatial co-expression as described below.

To construct the hierarchical clustering, voxels are spatially organized as a binary tree<sup>5</sup> where each node represents a collection of voxels and has zero or two branches (children). To initialize, all 51,533 voxels were assigned to the root node of the tree. As we descend the tree, a node is bifurcated into two nodes to achieve maximal dissimilarity between two groups of voxels based on correlation values. The bifurcation terminates whenever a node contains only a single voxel. This recursive division scheme is effectively multi-scale processing. The final tree consists of 103,065 nodes with a maximum depth of 53 levels and 51,533 leaf nodes (one for each voxel in the brain). At each bifurcation an ordering (albeit arbitrary) is assigned to each child to enable the definition a global “depth first” ordering for all leaf nodes.

Effective visualization of this large tree data structure is a challenging problem. A viewer has been implemented to provide an easy-to-use mechanism to navigate the tree, provide 3D context and visualize the multi-scale partitioning. Navigation works on the principle that from each leaf node there is only one path back to the root. To use the **Cluster** tool, a user selects a leaf node of the tree by choosing a voxel within the 3D reference volume and moves up and down the tree (along the root to leaf path) using the *Tree Depth* slider control below the cluster map. At each level of the tree, the voxels corresponding to the node can be browsed within its 3D spatial context.

The voxels of a node are visualized with a systematic color coding scheme. Each leaf node is assigned a global ordering such that each internal node of the tree represents voxels with a contiguously clustered ordering. All voxels of a node are then assigned a color based on the ‘jet’ color scheme where the leaf node with low order number is assigned shades of blue. The colors then run through green, yellow and orange. Finally, higher order voxels are assigned shades of red. Example visualizations are shown in **Supplementary Figure 3** for a leaf node within the medial group of the thalamus. Schematic coloring of the voxels by global ordering essentially provides a preview to the sub-tree organization. For the root node at *Tree Depth 0* (**Supplementary Fig. 3a**), coarse parcellation into gross anatomical structures can be observed while further down the tree at *Tree Depth 7* (**Supplementary Fig. 3b**), the arrangement of the colors indicates medial-lateral and rostral-caudal sub-organization in the thalamus.

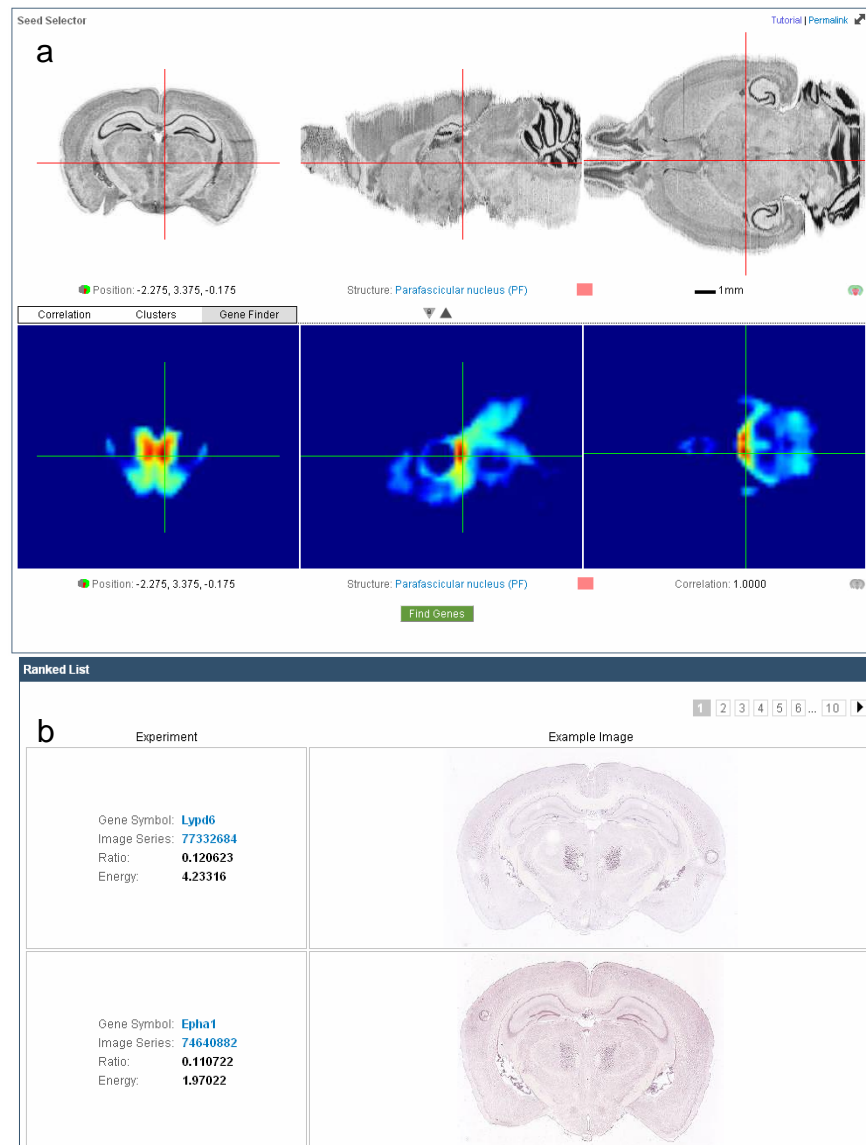


**Supplementary Figure 3. Two nodes in an expression-driven hierarchical spatial organization of the mouse brain.** Each coronal, sagittal, and horizontal image represents one node of a 3D data driven spatial clustering of the expression modes of the C57Bl/6J mouse brain. Each node in the decomposition tree represents a set of voxels and is visualized by a systematic color coding of the voxels using a “jet” color scheme. The colorization provides a preview to the sub-tree organization. **(a)** is the visualization of the root node spanning all voxels in the brain. Coarse parcellation into gross anatomical structures can be inferred from the colorization. The node in **(b)** spans the thalamus and colorization indicates a medial-lateral as well as a rostral-caudal gradient.

To make the creation of the tree computationally tractable, a multi-resolution approach was employed. Initially, a low-resolution tree was constructed by only considering one hemisphere and 1:8 sub-sampling (set A) resulting in a root node of 3738 voxels. Recursive bifurcation was performed for a few levels until all nodes contain less than 2000 voxels. At the next resolution level, more voxels are considered; spanning one hemisphere with 1:4 sub-sampling (set B) resulting in 7687 voxels. Voxels in set B which were not in set A are assigned to the same node as the highest correlated voxel within set (A/B). Recursive bifurcation is resumed until all nodes contain less than 1000 voxels. At the next stage more voxels are introduced to span one hemisphere with no sub-sampling (set C = 30,786). At the final stage all voxels from both hemispheres are used (set D = 51,533) and recursive bifurcation is performed until all leaf nodes represent a single voxel. Division at each node is done using the MATLAB (Mathworks, Natick, MA) implementation of hierarchical clustering using a “correlation” distance metric and an “average linkage” to generate the hierarchical tree.

**AGEA Gene Finder.** This tool enables users to search a local anatomic region of interest for genes within the ABA database that exhibit localized enrichment. Finding genes with highly localized expression patterns is of neuroscientific interest to study structural relationships and/or provide evidence for refinement of structural boundaries.

To use the **Gene Finder** tool, the user navigates to a voxel of interest in the reference atlas volume and a *fixed threshold* AGEA correlation map appears (described below in the Gene Finder Algorithm). By clicking on the “Find Genes” button a gene list from the ABA is returned. An example return page is shown in **Supplementary Figure 4b**. Note that the search facility operates on one fixed threshold. Both computational constraints and the practicalities of finding genes at every threshold level prevent arbitrary control of the threshold in the **Gene Finder** search.



**Supplementary Figure 4. Gene Finder search for seed location in the parafascicular nucleus (PF) of the thalamus. (a)** The seed voxel is selected by moving the red cross hair on the 3D Nissl atlas in the upper panels, a fixed threshold AGEA correlation map appears on the lower panels. Users click on “Find Genes” button to activate search. **(b)** Top two ranking genes from the enrichment ratio search. Return genes show enriched expression in the PF nucleus. Users can click on the example image to open up a multi-resolution image viewer or click on the image series number to see all the other images in the series. Clicking on the gene symbol will link them to information about the gene, probe and associated image series.

For each seed voxel, a fixed correlation threshold is pre-computed and the corresponding correlation map is displayed in the lower panel (**Supplementary Fig. 4a**). Voxels in the top third of the correlation range (orange to red voxels) form the local region of interest  $A$  and all voxels above threshold make up the domain or larger neighborhood  $B$  against which local specificity is to be measured. Images in the ABA database are ranked by the ratio of expression energy in  $A$  over expression energy in  $B$ . The top 200 ranked image series are returned for manual verification. The AGEA correlation map shown is selected to best represent the local correlation in the spatial neighborhood of the seed and is constructed as follows.

1. The computation proceeds independently for each of 16 regions  $R$  in the brain defined by unique intra-correlation patterns. These regions are approximately the cortex, hippocampus, striatum, thalamus, olfactory bulb, cerebellar cortex, hypothalamus, midbrain and hindbrain. Further, the ventricular areas, medial habenula, caudoputamen, deep cortical layers, olfactory nerve layer of the olfactory bulb, zona incerta and inferior olive are treated as specialized regions due their unique co-expression profiles. For each of these regions, a second “target domain” region  $R^+$  is also selected for determining the domain region  $B$  for specificity comparison. For example, for voxels in the cortex, we select the cortex as the specificity comparator. While for highly uniquely expressing areas such as the ventricles and medial habenula we select the whole brain as the specificity comparator. The regions  $R$  and  $R^+$  are defined using the AGEA binary tree clustering results.
2. For any initial seed  $s$  and correlation threshold value  $t$ , let  $N(t,s)$  denote the set of AGEA voxels whose correlation values  $\rho$  with the seed exceed  $t$ . In symbols,

$$N(t,s) = \{v_i : \rho(s, v_i) > t\}.$$

For each seed  $s$  in region  $R$ , we define an AGEA correlation region  $B(s)$  that most closely agrees with the target domain  $R^+$  by selecting an optimal threshold  $T$  chosen so that

$$T = \arg \max_t d(R^+, N(t,s))$$

where the distance metric  $d$  is defined as the Dice similarity metric (Dice similarity between two regions  $P$  and  $Q$  is given by  $(2 |P \cap Q| / (|P| + |Q|))$ ). The advantage of the Dice measure over simple intersection is that it also penalizes for differences in region size. Now let  $B(s) = N(T,s)$  represents the set of voxels exceeding this optimal threshold and is represented as the complete set of non-zero (non dark blue) rescaled voxels in **Supplementary Figure 4a**.

3. The most local neighborhood  $A(s)$  of highest correlated voxels with the seed  $s$ , (corresponding to the deepest orange-red colored voxels in **Supplementary Figure 4a** may be approximated by retrieving the voxels having highest correlation values from  $B(s)$ . Set

$$A(s) = \{v_j \in B(s) : \rho(v_j, s) > \rho'\}, \text{ where } \rho' = (T + 2)/3.$$

- Together the voxel sets  $A(s)$  and  $B(s)$  determine the local and larger anatomic context for AGEA correlation values centered at a fixed seed  $s$ . We can use the sets  $A(s)$  and  $B(s)$  to prioritize genes from the ABA in terms of how specific expression is to the local region as compared to the larger neighborhood. For a given gene  $g$  compute the expression energy  $E_g$  in both sets and define the  $E_{ratio}$  of the gene with respect to the seed  $s$  to be

$$E_{ratio}(g, s) = \frac{E_g(A(s))}{E_g(B(s))}$$

Values of the  $E_{ratio}$  range from 0.0 (not expressing in  $A(s)$ ) to 1.0 (ideal specificity to  $A(s)$ ) and genes can be ranked by descending values.

**Supplementary Figure 4b** shows two of the top gene returns for the given search together with their  $E_{ratio}$  and  $E_g(A(s))$ .

In the **Gene Finder** search false positives can result from dark artifacts and/or registration inaccuracies causing leakage of expression from neighboring regions of  $A(s)$ . The latter is particularly problematic when the region  $A(s)$  is near the boundary of the domain region  $B(s)$ . On the other hand, false negatives can occur from poor focusing, pale/white bubbles in the region of interest or alternatively dark artifacts and non-specific binding occurring in the domain region. Further, to eliminate false positives due to noise, an image series is only included in a list if the average energy in A is greater than 1. It may be possible that a gene with sparse and/or lighter intensity expression in the region of interest might be excluded by this criterion. A good analogy to AGEA **Gene Finder** would be an internet search engine where the user must further examine return results to find those most applicable to the query. Additionally, due to the nature of gene expression some brain areas have a large number of genes with robust expression while other areas have only a few genes and/or less robust expression.

**Multidimensional Scaling.** The clustering method employed in **Figure 6g** is a technique called multidimensional scaling (MDS)<sup>6, 7</sup>, and its goal is to provide a visual representation of the pattern of proximities, similarities, or distances amongst a set of objects. The input given in terms of a square matrix of inter object distances and the algorithm must find a set of coordinates in a Euclidean space of fixed input dimension  $d$  that respects the original distances. Often the plane  $\mathbb{R}^2$  is chosen for representation as it is the easiest to visualize. Usually an exact embedding of the data is not possible particularly if there are errors associated with the inter-point distances, however a correction procedure can be implemented such that the errors tend to cancel out. Any dataset of size  $n$  can be perfectly represented using  $n-1$  dimensions.

The MDS method is also known as *principal coordinate analysis* and is in particular closely related to principal components analysis<sup>7</sup>. There are two important observations about MDS maps. The first is that the axes are by themselves meaningless and the second is that the orientation of the picture is arbitrary. The MDS technique therefore identifies only a geometric realization of the data that respects the relative inter point distances. All that matters in an MDS map is which point is close to which others. In the representation of the data in **Figure 6f** inter point correlations alone give rise to the relationships between cortical layers and areas. Both laminar and areal organization is respected in **Figure 6g** but with a reorganization of relative areal structure.



The degree of correspondence between the distances among points implied by MDS map and the matrix input by the user is measured (inversely) by a *stress* function. A main consideration in using MDS is whether a true distance metric is respected by the inter point distances. In the case of inter area-layer domain correlations of **Figure 6f**, the triangle inequality of a distance metric may not be satisfied. In this case a modified version, non-metric MDS (nMDS), due to Kruskal<sup>6</sup> may be employed. We used the statistics toolbox for Matlab (Mathworks, Natick, MA) with default parameters in this implementation. This defaults to NON-METRIC MDS using Kruskal's normalized STRESS1 criterion for minimization. The formula is:

$$\sqrt{\frac{\sum \sum (f(x_{ij}) - d_{ij})^2}{\sum \sum d_{ij}^2}}$$

In the above equation,  $d_{ij}$  refers to the Euclidean distance, across all dimensions, between points  $i$  and  $j$  on the map,  $f(x_{ij})$  a function of the input data chosen for metric or non-metric MDS, and the term in the denominator refers to a constant scaling factor, used to keep stress values between 0 and 1. When the MDS map perfectly reproduces the input data,  $f(x_{ij}) - d_{ij}$  is for all  $i$  and  $j$ , so stress is zero. In general, smaller stresses lead to better representation. In metric scaling,  $f(x_{ij}) = x_{ij}$  and the raw input data is compared directly to the map distances. In non-metric scaling,  $f(x_{ij})$  is a weakly monotonic transformation of the input data that minimizes the stress function<sup>6</sup>.

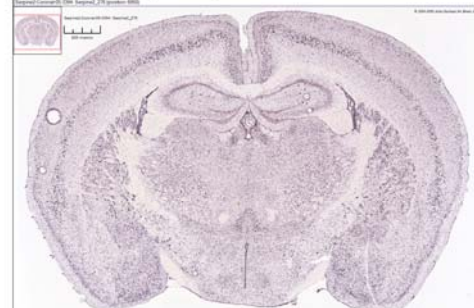
## **B. Supplementary Results**

### **Gene expression delineates cortical topography**

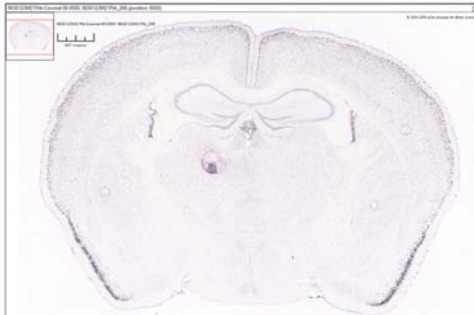
**a. Layer 1, A930038C07Rik**



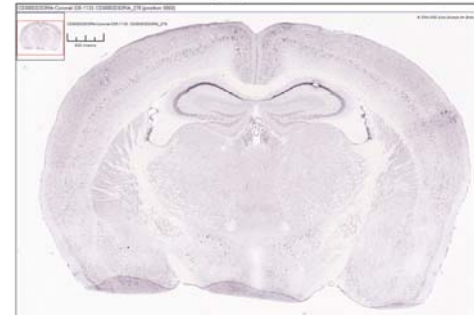
**e. Layer 5, Serpine2**



**b. Layer 2, 9830123M21Rik**



**f. Layer 5 (deep), C030003D03Rik**



**c. Layer 2/3, Rasgrf2**



**g. Layer 6, Cdh24**



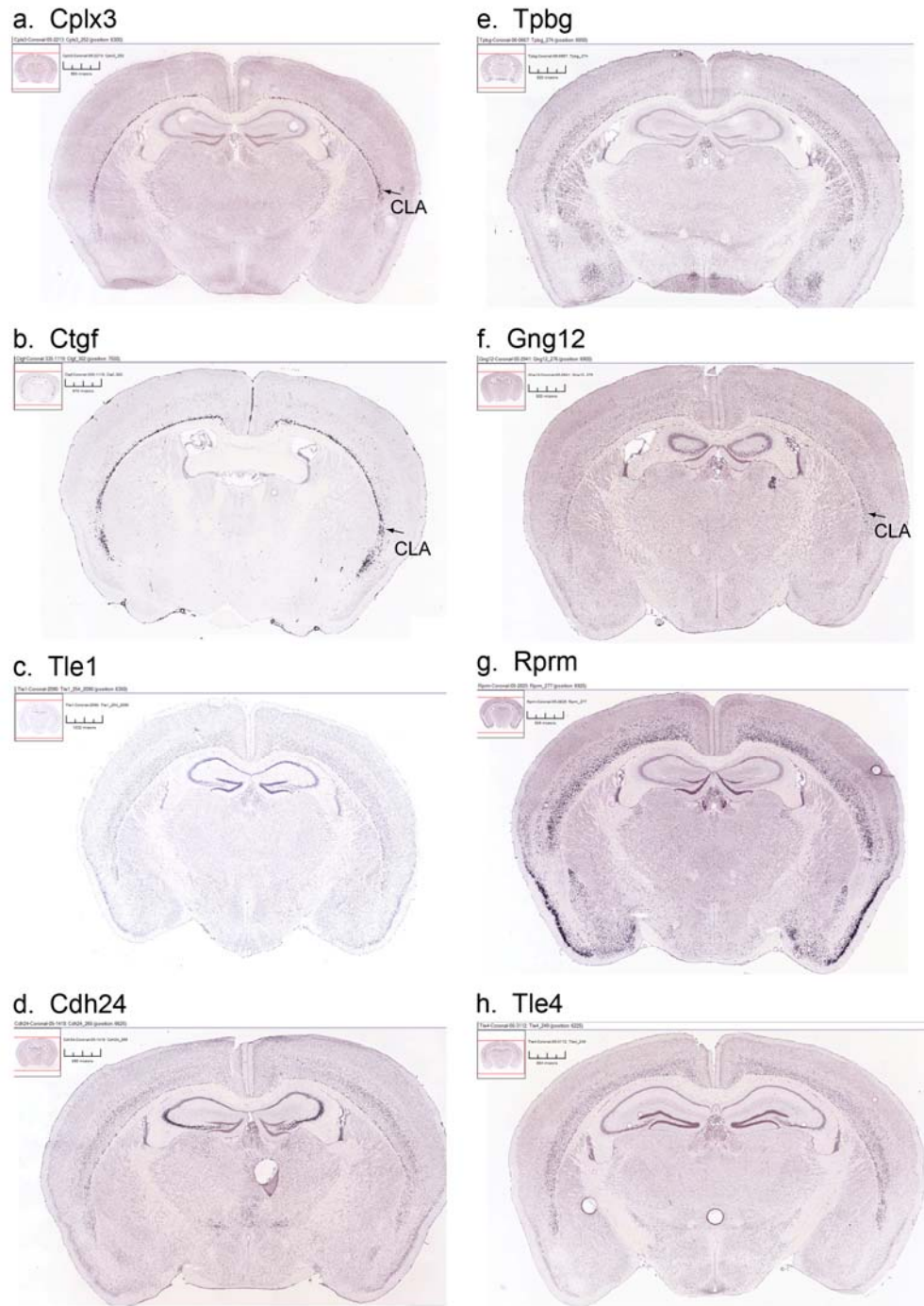
**d. Layer 3/4, LOC433228**



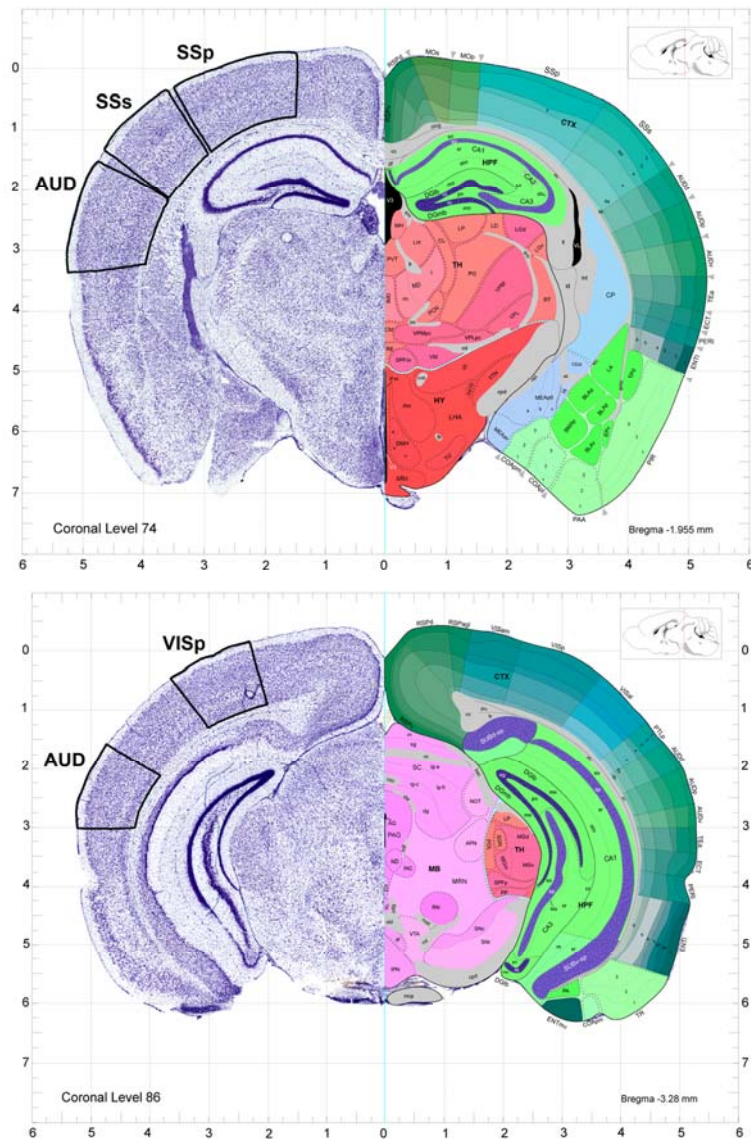
**h. Layer 6b, Cplx3**



**Supplementary Figure 5. Examples of cortical gene expression profiles in clusters derived from laminar divisions. ABA primary data can be found in hyperlinks listed in the links section.**



**Supplementary Figure 6. Laminar mode of gene expression in a cluster defined based upon enrichment in somatosensory cortex, layer 6b. Note co-expression with neighboring parts of the claustrum (CLA). ABA primary data can be found in hyperlinks listed in the links section.**



**Supplementary Figure 7. Annotation of AUD, SSp, SSs, and VISp in the Allen Reference Atlas on two sections at Bregma -1.955 and -3.28.** The location of auditory cortex (AUD), primary somatosensory cortex (SSp), secondary somatosensory cortex (SSs), and primary visual cortex (VISp) is indicated on the respective sections.

AGEA voxels	L2/3	L4	L5	L6a
AUD	103	37	112	68
SSp	427	180	394	313
SSs	74	40	79	75
VISp	88	39	76	47

**Supplementary Table 1. AGEA voxels for cortical area and layer.** Voxel count for each intersection of cortical area (left column) and layer (top row) reflects the relative size of 16 cortical domains containing seed points for AGEA data integration. Abbreviations: auditory (AUD), primary somatosensory (SSp), secondary somatosensory (SSs), primary visual (VISp), layers 2/3 (L2/3), layer 4 (L4), layer 5 (L5), and layer 6a (L6a).

The data presented in **Figure 6f** may be mathematically described as follows. For a given voxel  $v$  each AGEA map  $M_v$  summarizes the 3D correlations  $\rho(v, v')$  with each other voxel  $v'$ . By averaging the AGEA maps  $\{M_v : v \in D\}$  for a fixed domain  $D = A \cap L$  with area  $A$  and layer  $L$  (summing over voxel counts given in **Supplementary Table 1**) we may then compute the correlation between any two domains as

$$C(D', D'') = \frac{1}{|D'|} \frac{1}{|D''|} \sum_{v' \in D'} \sum_{v'' \in D''} \rho(v', v'')$$

which is clearly symmetric in  $D$  and  $D''$ . **Figure 6f** represents these pairwise averages as a colormap in which hot and cool colors represent higher and lower averaged correlation values. Actual correlation mean and standard deviation data is given in Supplementary Table 7. The values are organized as 4x4 blocks where each block represents the location of the seed domain as indicated by the upper and left side labels. The 4x4 sub-matrix within each block represents the location of the target domain as indicated by the lower and right side labels.

One would expect that the average correlation would be highest in the neighborhood of the seed domain. This is true in essentially all cases except for layer 5 SSp where the average correlation (0.9411) is less than the correlation in layer 6a SSp (0.9444). A (Welsch) t-test on Fisher normally transformed variates<sup>4</sup> is a comparison between (1.5766, 1.58127) with standard deviations (0.1410, 0.1079) on  $N=394$  with t value difference of -0.475 df = 612. The two-sided p-value of 0.6347 indicates that the result is not significant and probably due to variability in image.

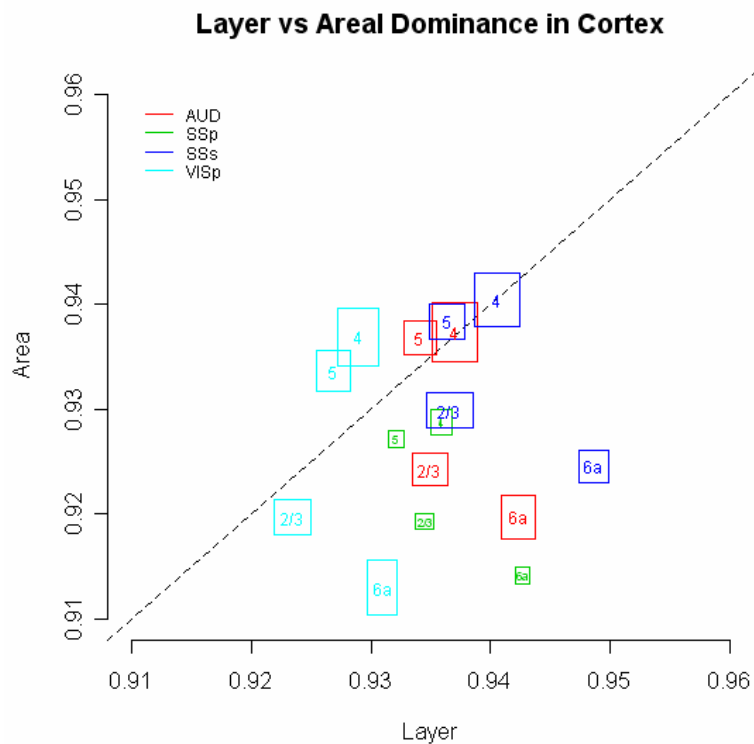
To measure the similarity of the co-expression profiles in **Figure 6f** across areas or layers we may form a vector of the data according to major area columns or major layer rows (length 64), that can be compared. The results presented in **Supplementary Table 2** show strong association of SSp and SSs beyond other regional associations. The data indicates correlation of AUD with other regions that is consistent with anatomic proximity, lower concordance of VISp with other regions indicating more of an outlier relationship. From the laminar perspective, adjacent layers have positive correlation of coexpression profile with the strongest concordance between layers 5 and 6a. For layers separated by others there is an increasing negative correlation inversely correlated with anatomic proximity.

Area/Layer	Area/Layer	Pearson CC
AUD	SSp	0.7655
AUD	SSs	0.7885
AUD	VISp	0.7163
SSp	SSs	0.9636
SSp	VISp	0.6286
SSs	VISp	0.5021
L2/3	L4	0.7390
L2/3	L5	-0.3022
L2/3	L6a	-0.5875
L4	L5	0.2929
L4	L6a	-0.2370
L5	L6a	0.8149

**Supplementary Table 2. Similarity of coexpression profiles for layers and regions.** Pearson correlation coefficient (CC) was computed by forming a vector of length 64 from each major area column or row layer. The vector is a summary coexpression profile across the cortex for seeds area or laminar seeds. Abbreviations: auditory cortex (AUD), primary somatosensory cortex (SSp), secondary somatosensory cortex (SSs), primary visual cortex (VISp), layer 2/3 (L2/3), layer 4 (L4), layer 5 (L5), layer 6a (L6a), degrees of freedom (df), and Pearson Correlation Coefficient (CC).

By averaging the data in **Figure 6f** over the corresponding row (area) and column (layer) containing that entry we have another measure of average areal or laminar correlation for seeds in that neighborhood. Similarly one may form the standard errors by averaging the corresponding standard deviations and using the seed counts from **Supplementary Table 1**. The results shown in **Supplementary Figure 8** are not strongly differential in absolute terms (range 0.92-0.96) although **Supplementary Figure 8** shows the general dominance of layers. In general, layer 2/3 and layer 6a exhibit universal dominance of layer over region with the strongest effect for layer 6a. The results for layers 4 and 5 are mixed with either ambiguous or even slight area dominance in the case of visual cortex. This interesting effect suggests that in visual cortex the regional areal effects of gene expression are more pronounced than in other cortical areas in that it is more likely to find a regionally expressed gene in primary visual cortex than in auditory or primary somatosensory cortex for which the effects of layers more heavily dominate.



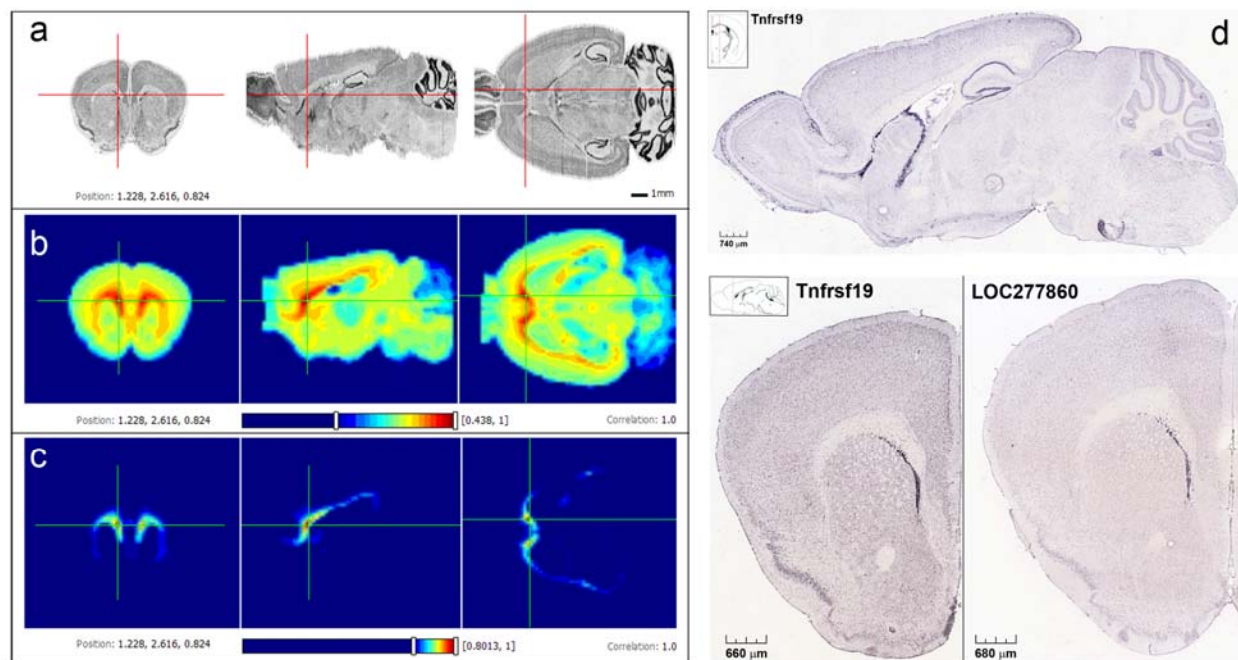


**Supplementary Figure 8. Laminar versus areal dominance in the cortex.** The data are derived by summing appropriate rows and columns from **Figure 6f** with corresponding standard errors. For each seed neighborhood an average layer and area correlation is obtained. The diagonal line represents equivalent laminar and areal effect. Abbreviations: auditory cortex (AUD), primary somatosensory cortex (SSp), secondary somatosensory cortex (SSs), and primary visual cortex (VISp).

## Characterization of a Neurogenic Domain

The expression correlation paradigm of AGEA shows that neurogenic domains such as the rostral migratory stream (RMS)<sup>8</sup>, which often present challenges for traditional atlas-based delineation, can be distinguished as neuroanatomical substructures based upon gene expression.

Selection of a seed voxel along the lateral ventricle of the right hemisphere (**Supplementary Fig. 9a**), consistent with the location of the RMS, reveals a distinct region of high co-expression running along the wall of the lateral ventricle, toward the hippocampus and rostrally toward the olfactory bulb (**Supplementary Fig. 9b**). Co-expression with the seed is notably low in areas such as the nucleus accumbens, red nucleus, cerebellum and thalamus. At a more restricted threshold, a dominant correlation cloud emerges along the ventricular walls, extending into the olfactory bulb, along the presumptive RMS track (**Supplementary Fig. 9c**). These 3D representations of correlated gene expression along the ventricular wall are consistent with numerous anatomical models of the RMS<sup>9</sup>, yet offer the first data-driven depiction of the RMS as a discrete anatomical unit extrapolated from gene expression.



**Supplementary Figure 9. AGEA delineating the RMS. (a)** Reference Nissl images reflecting coronal, sagittal and horizontal views. **(b)** Correlation maps from the selected seed point shown in the top row (Bregma 1.228, 2.616, 0.824) threshold range [0.438, 1]. **(c)** Restricted range [0.801, 1] highlights dominant correlation cloud along the ventricular walls and into the olfactory bulb, along the presumptive track of the RMS. **(d)** Illustrative RMS genes *Tnfrsf19* in sagittal and coronal plane, and *LOC277860* in coronal.

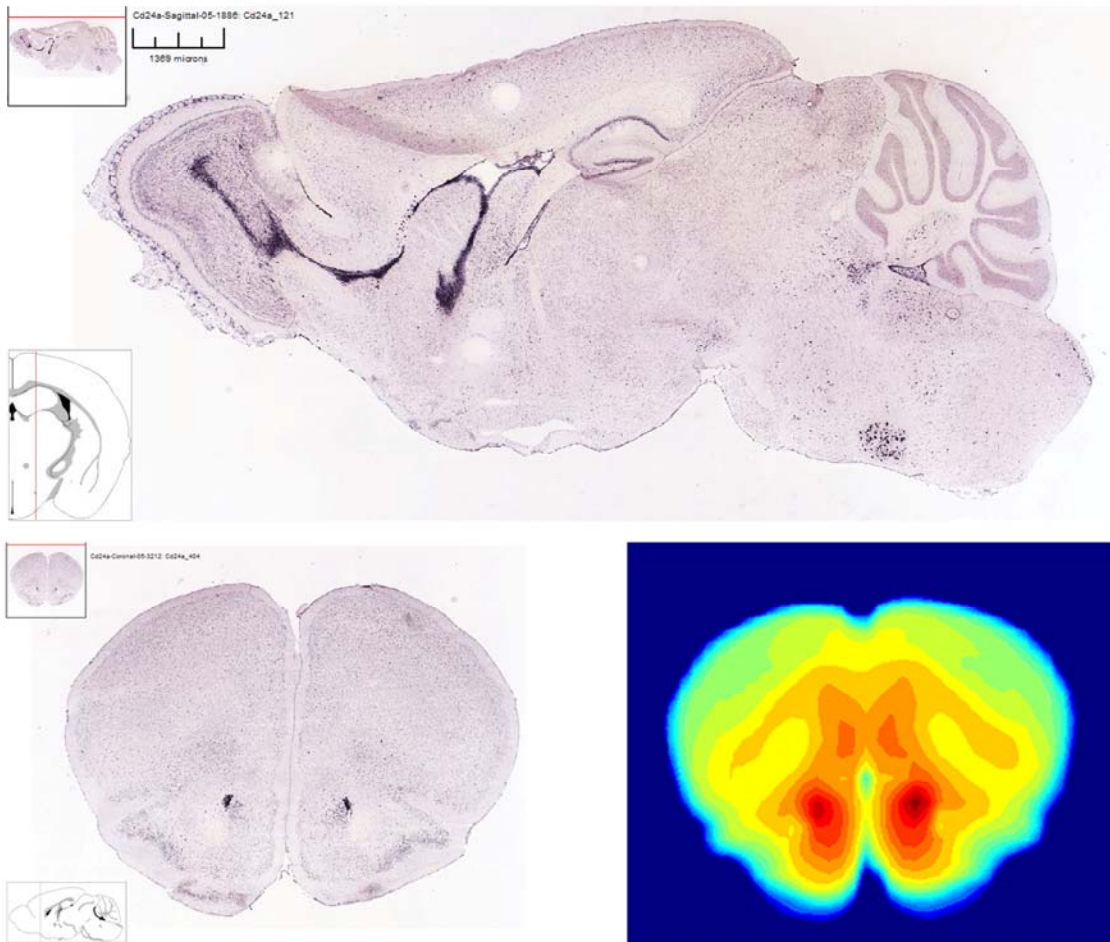
Correct development and functionality of the mammalian brain requires that postmitotic neurons migrate from the location of their birth origin to a terminal destination in the cortical plate. Migration of interneuron precursors, through functionally-defined structures such as the rostral migratory stream (RMS), contributes to expansion of neuronal populations in the olfactory bulb and other cortical regions, and is an example of neurogenesis and structural plasticity that persists throughout the life of the



animal, beyond early neurogenic developmental events. Areas that have been shown to be neurogenic in the adult brain include the dentate gyrus (DG) and the subventricular zone (SVZ), located on the wall of the lateral ventricle, which contributes to a cell-defined cytoarchitectural substructure RMS [For review, see<sup>9-11</sup>]. New neurons have also been found to migrate from the subgranular layer (SGL) to populate the granular zone of the DG. Non-neural ependymal cells that give rise to epithelial cells are also generated<sup>8</sup>. These processes have great interest for the role of neurogenesis in learning and memory, and models of disease and degeneration<sup>12</sup>. These neuroanatomic regions are notable in that they are comprised of nascent and migrating cells, and are thus defined by nonstatic, disparate cell types present in multiple structures that share a common functional profile: proliferation.

The nature of the RMS and other neurogenic areas is such that both neuronal and non-neuronal cells comingle, and these cells span multiple neuroanatomical boundaries. For this reason, it is difficult to delineate by traditional atlas-based approaches. Furthermore, accurate characterization using standard biological assays is challenged by its physical intercalation within heterogeneous structures and cell types, and thus *ex vivo* cell culture systems are often used<sup>13, 14</sup>. Implementing the correlational paradigms that are possible with AGEA, neurogenic domains such as the RMS can be distinguished as a neuroanatomical substructure, on the basis of gene expression.

*Gene Finder* can be used to identify genes representative of the RMS expression profile by placing a seed voxel within the rostral RMS. **Supplementary Table 3** list 50 manually verified returned genes with Entrez Gene identifiers and links to ABA ISH data. A biological process gene ontology (GO) analysis reveals a profile highly enriched in cell differentiation, cell migration, CNS development, neurogenesis, and other differentiation and development processes (**Supplementary Table 4**). One of these genes (*Cd24a*, shown in **Supplementary Fig. 10**, upper and lower left panels) is illustrative of the AGEA expression mode (**Supplementary Fig. 10**, lower right panel). A representative of this functional class, *Cd24a*, has been found to negatively regulate cell proliferation in zones of secondary neurogenesis and to regulate proliferation of neuronal precursors in the subventricular zone<sup>15</sup>.



**Supplementary Figure 10. Example result from a gene ontology query of highly-expressed genes in the RMS.** From *Gene Finder* search with seed voxel in the rostral RMS (Supplementary Table 3, and lower right panel), biological processes that are dominant for a subset of the genes correlating with the RMS profile generated by AGEA include neurogenesis, migration and cell differentiation. A sample gene expression image from the ABA (*Cd24a*, correlation = 0.798) derived from the seed profile characteristics is shown (top and lower left panels), alongside the AGEA seed heatmap (lower right panel).

Gene	Entrez ID	ABA Image Series ID	ABA URL
<i>Mdk</i>	17242	1227	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=50930&amp;coordSystem=pixel&amp;x=4640&amp;y=2280&amp;z=8.62068965517241">http://mouse.brain-map.org:80/viewImage.do?imageId=50930&amp;coordSystem=pixel&amp;x=4640&amp;y=2280&amp;z=8.62068965517241</a>
<i>Cd24a</i>	12484	73787950	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=70400133&amp;coordSystem=pixel&amp;x=7384.5&amp;y=3768.5&amp;z=5.41675130340578">http://mouse.brain-map.org:80/viewImage.do?imageId=70400133&amp;coordSystem=pixel&amp;x=7384.5&amp;y=3768.5&amp;z=5.41675130340578</a>
<i>Rrm2</i>	20135	74272039	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=69759546&amp;coordSystem=pixel&amp;x=7368.5&amp;y=3808.5&amp;z=5.42851326592929">http://mouse.brain-map.org:80/viewImage.do?imageId=69759546&amp;coordSystem=pixel&amp;x=7368.5&amp;y=3808.5&amp;z=5.42851326592929</a>
<i>Ccnd2</i>	12444	205	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=97563&amp;coordSystem=pixel&amp;x=4400&amp;y=2850&amp;z=9.09090909090909">http://mouse.brain-map.org:80/viewImage.do?imageId=97563&amp;coordSystem=pixel&amp;x=4400&amp;y=2850&amp;z=9.09090909090909</a>
<i>Dlx1</i>	13390	348	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=91331&amp;coordSystem=pixel&amp;x=4540&amp;y=2360&amp;z=8.81057268722467">http://mouse.brain-map.org:80/viewImage.do?imageId=91331&amp;coordSystem=pixel&amp;x=4540&amp;y=2360&amp;z=8.81057268722467</a>
<i>Mcm6</i>	17219	71358638	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=68702662&amp;coordSystem=pixel&amp;x=7608.5&amp;y=3248.5&amp;z=5.25727804429257">http://mouse.brain-map.org:80/viewImage.do?imageId=68702662&amp;coordSystem=pixel&amp;x=7608.5&amp;y=3248.5&amp;z=5.25727804429257</a>
<i>Dlx2</i>	13392	1482	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=50249&amp;coordSystem=pixel&amp;x=4496&amp;y=2312&amp;z=8.89679715302491">http://mouse.brain-map.org:80/viewImage.do?imageId=50249&amp;coordSystem=pixel&amp;x=4496&amp;y=2312&amp;z=8.89679715302491</a>
<i>Shhrs</i>	320038	2000	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=10034&amp;coordSystem=pixel&amp;x=4812&amp;y=2932&amp;z=8.31255195344971">http://mouse.brain-map.org:80/viewImage.do?imageId=10034&amp;coordSystem=pixel&amp;x=4812&amp;y=2932&amp;z=8.31255195344971</a>
<i>Hist1h1b</i>	56702	74272040	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=70430078&amp;coordSystem=pixel&amp;x=7008.5&amp;y=3328.5&amp;z=5.70735535421274">http://mouse.brain-map.org:80/viewImage.do?imageId=70430078&amp;coordSystem=pixel&amp;x=7008.5&amp;y=3328.5&amp;z=5.70735535421274</a>

<i>Hist1h1a</i>	80838	74988764	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=70430027&amp;coordSystem=pixel&amp;x=7360.5&amp;y=3784.5&amp;z=5.43441342300115">http://mouse.brain-map.org:80/viewImage.do?imageId=70430027&amp;coordSystem=pixel&amp;x=7360.5&amp;y=3784.5&amp;z=5.43441342300115</a>
<i>Top2a</i>	21973	1301	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=54980&amp;coordSystem=pixel&amp;x=4624&amp;y=2268&amp;z=8.65051903114187">http://mouse.brain-map.org:80/viewImage.do?imageId=54980&amp;coordSystem=pixel&amp;x=4624&amp;y=2268&amp;z=8.65051903114187</a>
<i>Rps5</i>	20103	907	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=77482296&amp;coordSystem=pixel&amp;x=7688.5&amp;y=4272.5&amp;z=5.20257527476101">http://mouse.brain-map.org:80/viewImage.do?imageId=77482296&amp;coordSystem=pixel&amp;x=7688.5&amp;y=4272.5&amp;z=5.20257527476101</a>
<i>Ckap2</i>	80986	74363353	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=72583717&amp;coordSystem=pixel&amp;x=7008.5&amp;y=3800.5&amp;z=5.70735535421274">http://mouse.brain-map.org:80/viewImage.do?imageId=72583717&amp;coordSystem=pixel&amp;x=7008.5&amp;y=3800.5&amp;z=5.70735535421274</a>
<i>LOC277860</i>	277860	74581425	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=71495464&amp;coordSystem=pixel&amp;x=7440.5&amp;y=4120.5&amp;z=5.37598279685505">http://mouse.brain-map.org:80/viewImage.do?imageId=71495464&amp;coordSystem=pixel&amp;x=7440.5&amp;y=4120.5&amp;z=5.37598279685505</a>
<i>Dbi</i>	13167	71836880	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=68212431&amp;coordSystem=pixel&amp;x=8304.5&amp;y=3752.5&amp;z=4.81666566319465">http://mouse.brain-map.org:80/viewImage.do?imageId=68212431&amp;coordSystem=pixel&amp;x=8304.5&amp;y=3752.5&amp;z=4.81666566319465</a>
<i>Dpysl5</i>	65254	73635770	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=71433361&amp;coordSystem=pixel&amp;x=7488.5&amp;y=3832.5&amp;z=5.34152366962676">http://mouse.brain-map.org:80/viewImage.do?imageId=71433361&amp;coordSystem=pixel&amp;x=7488.5&amp;y=3832.5&amp;z=5.34152366962676</a>
<i>Thbs4</i>	21828	71670699	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=69910902&amp;coordSystem=pixel&amp;x=7632.5&amp;y=3872.5&amp;z=5.24074680641992">http://mouse.brain-map.org:80/viewImage.do?imageId=69910902&amp;coordSystem=pixel&amp;x=7632.5&amp;y=3872.5&amp;z=5.24074680641992</a>
<i>Mki67</i>	17345	1381	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=46407&amp;coordSystem=pixel&amp;x=4684&amp;y=2428&amp;z=8.5397096498719">http://mouse.brain-map.org:80/viewImage.do?imageId=46407&amp;coordSystem=pixel&amp;x=4684&amp;y=2428&amp;z=8.5397096498719</a>
<i>Sox2</i>	20674	77280331	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=79682350&amp;coordSystem=pixel&amp;x=7400.5&amp;y=3784.5&amp;z=5.40504019998649">http://mouse.brain-map.org:80/viewImage.do?imageId=79682350&amp;coordSystem=pixel&amp;x=7400.5&amp;y=3784.5&amp;z=5.40504019998649</a>
<i>Spag16</i>	66722	75080199	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=71775235&amp;coordSystem=pixel&amp;x=7328.5&amp;y=3928.5&amp;z=5.45814286688954">http://mouse.brain-map.org:80/viewImage.do?imageId=71775235&amp;coordSystem=pixel&amp;x=7328.5&amp;y=3928.5&amp;z=5.45814286688954</a>
<i>Scara3</i>	219151	75042270	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=69601695&amp;coordSystem=pixel&amp;x=7304.5&amp;y=3808.5&amp;z=5.47607639126566">http://mouse.brain-map.org:80/viewImage.do?imageId=69601695&amp;coordSystem=pixel&amp;x=7304.5&amp;y=3808.5&amp;z=5.47607639126566</a>
<i>Sp8</i>	320145	74272904	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=71883600&amp;coordSystem=pixel&amp;x=7456.5&amp;y=3880.5&amp;z=5.36444712666801">http://mouse.brain-map.org:80/viewImage.do?imageId=71883600&amp;coordSystem=pixel&amp;x=7456.5&amp;y=3880.5&amp;z=5.36444712666801</a>
<i>Kif5a</i>	16572	2351	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=130737&amp;coordSystem=pixel&amp;x=4712&amp;y=2556&amp;z=8.48896434634974">http://mouse.brain-map.org:80/viewImage.do?imageId=130737&amp;coordSystem=pixel&amp;x=4712&amp;y=2556&amp;z=8.48896434634974</a>
<i>Sall3</i>	20689	74363352	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=72583113&amp;coordSystem=pixel&amp;x=7312.5&amp;y=4000.5&amp;z=5.47008547008547">http://mouse.brain-map.org:80/viewImage.do?imageId=72583113&amp;coordSystem=pixel&amp;x=7312.5&amp;y=4000.5&amp;z=5.47008547008547</a>
<i>Islr2</i>	320563	142	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=4362&amp;coordSystem=pixel&amp;x=4452&amp;y=2536&amp;z=8.98472596585804">http://mouse.brain-map.org:80/viewImage.do?imageId=4362&amp;coordSystem=pixel&amp;x=4452&amp;y=2536&amp;z=8.98472596585804</a>
<i>Nfix</i>	18032	2423	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=77612025&amp;coordSystem=pixel&amp;x=7216.5&amp;y=3712.5&amp;z=5.5428531836763">http://mouse.brain-map.org:80/viewImage.do?imageId=77612025&amp;coordSystem=pixel&amp;x=7216.5&amp;y=3712.5&amp;z=5.5428531836763</a>
<i>Syncrip</i>	56403	1391	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=46847&amp;coordSystem=pixel&amp;x=4420&amp;y=2260&amp;z=9.04977375565611">http://mouse.brain-map.org:80/viewImage.do?imageId=46847&amp;coordSystem=pixel&amp;x=4420&amp;y=2260&amp;z=9.04977375565611</a>
<i>Cspg2</i>	13003	73520975	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=69552735&amp;coordSystem=pixel&amp;x=7512.5&amp;y=3808.5&amp;z=5.32445923460898">http://mouse.brain-map.org:80/viewImage.do?imageId=69552735&amp;coordSystem=pixel&amp;x=7512.5&amp;y=3808.5&amp;z=5.32445923460898</a>
<i>2610109H07Rik</i>	70433	74272038	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=70238355&amp;coordSystem=pixel&amp;x=7648.5&amp;y=4024.5&amp;z=5.22978361770282">http://mouse.brain-map.org:80/viewImage.do?imageId=70238355&amp;coordSystem=pixel&amp;x=7648.5&amp;y=4024.5&amp;z=5.22978361770282</a>
<i>Btg1</i>	12226	73718576	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=71467062&amp;coordSystem=pixel&amp;x=7184.5&amp;y=3360.5&amp;z=5.56754123460227">http://mouse.brain-map.org:80/viewImage.do?imageId=71467062&amp;coordSystem=pixel&amp;x=7184.5&amp;y=3360.5&amp;z=5.56754123460227</a>
<i>Pola1</i>	18968	75084100	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=69745874&amp;coordSystem=pixel&amp;x=7288.5&amp;y=3848.5&amp;z=5.48809768813885">http://mouse.brain-map.org:80/viewImage.do?imageId=69745874&amp;coordSystem=pixel&amp;x=7288.5&amp;y=3848.5&amp;z=5.48809768813885</a>
<i>Nfia</i>	18027	1239	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=51975&amp;coordSystem=pixel&amp;x=4572&amp;y=2896&amp;z=8.74890638670166">http://mouse.brain-map.org:80/viewImage.do?imageId=51975&amp;coordSystem=pixel&amp;x=4572&amp;y=2896&amp;z=8.74890638670166</a>
<i>Samd14</i>	217125	73930839	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=70196770&amp;coordSystem=pixel&amp;x=7504.5&amp;y=4184.5&amp;z=5.33013525218202">http://mouse.brain-map.org:80/viewImage.do?imageId=70196770&amp;coordSystem=pixel&amp;x=7504.5&amp;y=4184.5&amp;z=5.33013525218202</a>
<i>Hist1h2bc</i>	68024	560	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=86560&amp;coordSystem=pixel&amp;x=4616&amp;y=2384&amp;z=8.66551126516464">http://mouse.brain-map.org:80/viewImage.do?imageId=86560&amp;coordSystem=pixel&amp;x=4616&amp;y=2384&amp;z=8.66551126516464</a>
<i>Arx</i>	11878	118	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=3633&amp;coordSystem=pixel&amp;x=4348&amp;y=2820&amp;z=9.19963201471941">http://mouse.brain-map.org:80/viewImage.do?imageId=3633&amp;coordSystem=pixel&amp;x=4348&amp;y=2820&amp;z=9.19963201471941</a>
<i>Gldc</i>	104174	77887886	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=79330513&amp;coordSystem=pixel&amp;x=8320.5&amp;y=3824.5&amp;z=4.80740340123791">http://mouse.brain-map.org:80/viewImage.do?imageId=79330513&amp;coordSystem=pixel&amp;x=8320.5&amp;y=3824.5&amp;z=4.80740340123791</a>
<i>Foxg1</i>	15228	2230	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=9356&amp;coordSystem=pixel&amp;x=4452&amp;y=2352&amp;z=8.98472596585804">http://mouse.brain-map.org:80/viewImage.do?imageId=9356&amp;coordSystem=pixel&amp;x=4452&amp;y=2352&amp;z=8.98472596585804</a>
<i>Igfbp5</i>	16011	73592530	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=69629679&amp;coordSystem=pixel&amp;x=7416.5&amp;y=3960.5&amp;z=5.39337962650846">http://mouse.brain-map.org:80/viewImage.do?imageId=69629679&amp;coordSystem=pixel&amp;x=7416.5&amp;y=3960.5&amp;z=5.39337962650846</a>
<i>Id4</i>	15904	74357547	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=72581601&amp;coordSystem=pixel&amp;x=7288.5&amp;y=4280.5&amp;z=5.48809768813885">http://mouse.brain-map.org:80/viewImage.do?imageId=72581601&amp;coordSystem=pixel&amp;x=7288.5&amp;y=4280.5&amp;z=5.48809768813885</a>
<i>Nnat</i>	18111	655497	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=77734325&amp;coordSystem=pixel&amp;x=7736.5&amp;y=3928.5&amp;z=5.17029664577005">http://mouse.brain-map.org:80/viewImage.do?imageId=77734325&amp;coordSystem=pixel&amp;x=7736.5&amp;y=3928.5&amp;z=5.17029664577005</a>
<i>Tnfrsf19</i>	29820	74425524	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=75569659&amp;coordSystem=pixel&amp;x=7272.5&amp;y=3664.5&amp;z=5.50017188037126">http://mouse.brain-map.org:80/viewImage.do?imageId=75569659&amp;coordSystem=pixel&amp;x=7272.5&amp;y=3664.5&amp;z=5.50017188037126</a>
<i>Grid2ip</i>	170935	71670479	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=69540057&amp;coordSystem=pixel&amp;x=7496.5&amp;y=3688.5&amp;z=5.33582338424598">http://mouse.brain-map.org:80/viewImage.do?imageId=69540057&amp;coordSystem=pixel&amp;x=7496.5&amp;y=3688.5&amp;z=5.33582338424598</a>
<i>Zfx2as</i>	432855	74363340	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=72161467&amp;coordSystem=pixel&amp;x=7608.5&amp;y=3824.5&amp;z=5.25727804429257">http://mouse.brain-map.org:80/viewImage.do?imageId=72161467&amp;coordSystem=pixel&amp;x=7608.5&amp;y=3824.5&amp;z=5.25727804429257</a>
<i>Rps12</i>	20042	70928395	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=597034&amp;coordSystem=pixel&amp;x=7024.5&amp;y=3824.5&amp;z=5.69435547014022">http://mouse.brain-map.org:80/viewImage.do?imageId=597034&amp;coordSystem=pixel&amp;x=7024.5&amp;y=3824.5&amp;z=5.69435547014022</a>
<i>Dchs1</i>	233651	72472786	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=69382270&amp;coordSystem=pixel&amp;x=7272.5&amp;y=3688.5&amp;z=5.50017188037126">http://mouse.brain-map.org:80/viewImage.do?imageId=69382270&amp;coordSystem=pixel&amp;x=7272.5&amp;y=3688.5&amp;z=5.50017188037126</a>
<i>Ptpnz1</i>	19283	77371825	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=71290524&amp;coordSystem=pixel&amp;x=7416.5&amp;y=3440.5&amp;z=5.39337962650846">http://mouse.brain-map.org:80/viewImage.do?imageId=71290524&amp;coordSystem=pixel&amp;x=7416.5&amp;y=3440.5&amp;z=5.39337962650846</a>
<i>Ascl1</i>	17172	73817423	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=71519775&amp;coordSystem=pixel&amp;x=7552.5&amp;y=3736.5&amp;z=5.29625951671632">http://mouse.brain-map.org:80/viewImage.do?imageId=71519775&amp;coordSystem=pixel&amp;x=7552.5&amp;y=3736.5&amp;z=5.29625951671632</a>
<i>B230114H05Rik</i>		75043139	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=73772128&amp;coordSystem=pixel&amp;x=7344.5&amp;y=3712.5&amp;z=5.44625229763769">http://mouse.brain-map.org:80/viewImage.do?imageId=73772128&amp;coordSystem=pixel&amp;x=7344.5&amp;y=3712.5&amp;z=5.44625229763769</a>
<i>Vav2</i>	22325	74583149	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=68338452&amp;coordSystem=pixel&amp;x=7432.5&amp;y=4112.5&amp;z=5.38176925664312">http://mouse.brain-map.org:80/viewImage.do?imageId=68338452&amp;coordSystem=pixel&amp;x=7432.5&amp;y=4112.5&amp;z=5.38176925664312</a>
<i>Dpysl3</i>	22240	654928	<a href="http://mouse.brain-map.org:80/viewImage.do?imageId=71432654&amp;coordSystem=pixel&amp;x=7376.5&amp;y=3728.5&amp;z=5.42262590659527">http://mouse.brain-map.org:80/viewImage.do?imageId=71432654&amp;coordSystem=pixel&amp;x=7376.5&amp;y=3728.5&amp;z=5.42262590659527</a>

**Supplementary Table 3. Fifty returned genes from Gene Finder search with a seed in the rostral RMS.**

A thresholded correlation map is used as a template to search the ABA database. The Entrez Gene ID, ABA Image Series ID and ABA URL are shown for each gene.

Gene ontology term (DAVID)	Number of genes	Percent of gene list	P-value
Development	19	39.6	2.20E-06
Nuclear protein	17	35.4	2.00E-05
DNA binding	15	31.2	1.40E-08
Cell differentiation	11	22.9	1.20E-04
Nervous system development	9	18.8	5.60E-05
Developmental protein	8	16.7	4.50E-05
Alternative splicing	8	16.7	7.80E-02
Transcriptional regulation	8	16.7	7.20E-03
Transcription	7	14.6	2.20E-02
Phosphorylation	7	14.6	7.80E-02
Neurogenesis	6	12.5	8.50E-04
Neuron differentiation	5	10.4	4.30E-03
Direct protein sequencing	5	10.4	2.10E-02
DNA replication	5	10.4	5.20E-06
Central nervous system development	4	8.3	6.40E-03
Acetylation	4	8.3	2.00E-02
Differentiation	3	6.2	7.70E-02
Ribonucleoprotein	3	6.2	6.80E-02
Cell cycle control	2	4.2	5.00E-02

**Supplementary Table 4. Gene ontology analysis of genes representative of the RMS expression profile.** Gene ontology (GO) analysis from DAVID of the gene list in **Supplementary Table 3** yields genes rich in the biological processes of neurogenesis, migration and cell differentiation. Overall gene count, percent of genes in each category, and p-value are given<sup>16</sup>.

Gene Symbol	Gene Name	Image Series ID	Entrez Gene ID	NCBI Accession
Sept5	septin 5	958	18951	NM_213614
Sept7	septin 7	961	235072	NM_009859
0610007P14Rik	RIKEN cDNA 0610007P14 gene	70927828	58520	NM_021446.1
0610009A07Rik	iodotyrosine deiodinase	71015205	70337	NM_027391.1
0610009I22Rik	cardiolipin synthase 1	1148	66586	NM_025646
0610009M14Rik	TSC22 domain family 4	1464		NM_023910
0610010D24Rik	coiled-coil domain containing 88C	74363346	68339	NM_026681.3
0610010F05Rik	RIKEN cDNA 0610010F05 gene	74957923	71675	NM_027860.1
0610010O12Rik	RIKEN cDNA 0610010O12 gene	75079788	66060	XM_488847.1
0610011I04Rik	transmembrane protein 176A	75650863	66058	NM_025326.2
0610011I04Rik	transmembrane protein 176A	70813929	66058	NM_025326.2
0610016J10Rik	mediator of cell motility 1	1942	76890	NM_133771
0610042C05Rik	required for meiotic nuclear division 1 homolog (S. cerevisiae)	77371805	66084	NM_025343.2
0710001E13Rik	cyclic AMP-regulated phosphoprotein, 21	71587781	74100	NM_028755.2
0710005M24Rik	RALY RNA binding protein-like	72129250	76897	NM_178631.2
1110002B05Rik	RIKEN cDNA 1110002B05 gene	72081396	104725	NM_134054.1
1110003F05Rik	RIKEN cDNA 1110003F05 gene	1150	66145	
1110006I15Rik	transmembrane protein 109	74988461	68539	NM_134142.1
1110007C09Rik	RIKEN cDNA 1110007C09 gene	74357561	68480	NM_026738.1
1110008L20Rik	EF hand domain family A1	1946		NM_028643
1110008P14Rik	RIKEN cDNA 1110008P14 gene	71015816	73737	NM_198001.1
1110014F12Rik	tetraspanin 11	70436731	68498	NM_026743.2
1110019N10Rik	RIKEN cDNA 1110019N10 gene	74819685	68523	NM_026753.1
1110019O13Rik	LETM1 domain containing 1	1635		NM_134093
1110021D20Rik	glycosyltransferase 8 domain containing 2	71249079	74782	XM_483930.1
1110021H02Rik	ubiquitin-fold modifier conjugating enzyme 1	1637		NM_025388
1110031B06Rik	RIKEN cDNA 1110031B06 gene	3	67826	NM_144521
1110033J19Rik	ribosomal protein S4, Y-linked 2	75934917	66184	NM_025405.1
1110036O03Rik	RIKEN cDNA 1110036O03 gene	2547	66180	NM_176830
1110037F02Rik	RIKEN cDNA 1110037F02 gene	74988462	66185	XM_283937.3
1110049B09Rik	RIKEN cDNA 1110049B09 gene	74272042	68764	XM_126902.3
1110059H15Rik	zinc finger protein 650	74988721	68795	XM_485005.1
1110061A14Rik	RIKEN cDNA 1110061A14 gene	1313	68827	
1110064P04Rik	AHA1, activator of heat shock protein ATPase homolog 2 (yeast)	71358552	268390	NM_172391.2
1110069I04Rik		75144656		
1190002N15Rik	RIKEN cDNA 1190002N15 gene	77332088	68861	XM_147036.5
1190003M12Rik	RIKEN cDNA 1190003M12 gene	74957933	68888	XM_355795.1
1200002G13Rik	transmembrane emp24 domain containing 3	71015196	66111	NM_025360.1
1200003E16Rik	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	72081515	66860	XM_130249.4
1200007D18Rik	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	1952	67458	NM_026170
1200011I18Rik	RIKEN cDNA 1200011I18 gene	293464	67467	NM_026177.2
1200011I18Rik	RIKEN cDNA 1200011I18 gene	77414569	67467	NM_026177.2
1200016E24Rik	RIKEN cDNA 1200016E24 gene	1591	319202	XM_489305
1200016G03Rik	keratin 80	74724762	74127	XM_283319.3
1300006C19Rik	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	71020390	68292	XM_358385.2
1300007L22Rik	shroom family member 1	1315	71774	NM_027917
1300010A20Rik	tetraspanin 33	70743905	232670	NM_146173.1

1300013D05Rik	coiled-coil domain containing 49	73929874	67480	NM_026186.2
1500002O20Rik	RIKEN cDNA 1500002O20 gene	1954	71997	NM_028047
1500019G21Rik	RIKEN cDNA 1500019G21 gene	75774674	66245	NM_024172.2
1500026D16Rik	ribonuclease H2, subunit C	67870083	68209	NM_026616.1
1500032D16Rik	RIKEN cDNA 1500032D16 gene	12	78330	NM_030087
1500032L24Rik	RIKEN cDNA 1500032L24 gene	75651168	69029	XM_193800.3
1600015H20Rik	RIKEN cDNA 1600015H20 gene	73929875	70370	NM_024237.2
1700001E04Rik	RIKEN cDNA 1700001E04 gene	73929885	75438	NM_029288.1
1700007D05Rik	MTERF domain containing 3	70231999	74238	NM_028832.1
1700010C24Rik	RIKEN cDNA 1700010C24 gene	74581399	70363	NM_027401.1
1700019N12Rik	RIKEN cDNA 1700019N12 gene	73718050	67077	NM_025953.1
1700019N12Rik	RIKEN cDNA 1700019N12 gene	75233110	67077	NM_025953.1
1700020C11Rik	RIKEN cDNA 1700020C11 gene	75774673	67900	NM_026443.2
1700026G02Rik	A kinase (PRKA) anchor protein 13	74581373	75547	XM_485950.1
1700037H04Rik	RIKEN cDNA 1700037H04 gene	324211	67326	NM_026091.1
1700054N08Rik	RIKEN cDNA 1700054N08 gene	70743908	73420	XM_134542.3
1700086L19Rik	RIKEN cDNA 1700086L19 gene	1643	74284	XM_358420
1700086L19Rik	RIKEN cDNA 1700086L19 gene	14	74284	XM_358420
1810009M01Rik	transmembrane protein 176B	2103	65963	NM_023056
1810009M01Rik	transmembrane protein 176B	77866852	65963	NM_023056.2
1810015C04Rik	RIKEN cDNA 1810015C04 gene	70634224	66270	NM_025459.2
1810015M01Rik	TP53 regulated inhibitor of apoptosis 1	74658242	69076	NM_026933.1
1810020D17Rik	RIKEN cDNA 1810020D17 gene	1958	66273	NM_183251
1810020E01Rik	transmembrane protein 126A	276072	66271	NM_025460.1
1810021J13Rik	RIKEN cDNA 1810021J13 gene	1960	66279	NM_025464
1810023C24Rik		77340486		
1810030J14Rik	RIKEN cDNA 1810030J14 gene	1962	66289	NM_025470
1810031K17Rik	RIKEN cDNA 1810031K17 gene	227165	69171	NM_026977.1
1810041L15Rik	RIKEN cDNA 1810041L15 gene	72340125	72301	XM_128169.5
1810045K07Rik	transmembrane protein 66	70743884	67887	NM_026432.2
1810048P08Rik	RAB43, member RAS oncogene family	73929886	69834	NM_133717.1
1810057P16Rik	matrix-remodelling associated 7	77332080	67622	XM_126676.3
1810058I14Rik	Ndufa12-like	74988362	75597	XM_484315.1
1810060J02Rik	coiled-coil domain containing 91	74818623	67015	NM_025911.1
1810073G14Rik	RIKEN cDNA 1810073G14 gene	1992	67726	NM_026342
2010004A03Rik	RIKEN cDNA 2010004A03 gene	72007750	76527	NM_029646.1
2010008E23Rik	transmembrane and ubiquitin-like domain containing 2	293027	72053	XM_126502.5
2010106G01Rik	RIKEN cDNA 2010106G01 gene	1647	66552	NM_023220
2010300C02Rik	RIKEN cDNA 2010300C02 gene	70743898	72097	XM_129808.4
2010309E21Rik	RIKEN cDNA 2010309E21 gene	1964	66488	NM_025591
2210010A19Rik	pyridoxal-dependent decarboxylase domain containing 1	77869146	94184	NM_053181.1
2210010L05Rik	RIKEN cDNA 2210010L05 gene	75651167	98682	NM_133829.1
2210403B10Rik	RAS-like, family 10, member A	73636038	75668	NM_145216.2
2210407G14Rik		73930821	72378	XM_148399.5
2210415K24Rik	G protein-coupled receptor associated sorting protein 1	70743888	67298	NM_001004359.0
2300002D11Rik	RIKEN cDNA 2300002D11 gene	72080175	69539	XM_149530.4
2310001H12Rik	RIKEN cDNA 2310001H12 gene	75774665	69504	NM_145563.1
2310003H01Rik	RIKEN cDNA 2310003H01 gene	72080185	71885	XM_126658.4
2310004L02Rik	RIKEN cDNA 2310004L02 gene	75773705	66349	NM_025504.2

2310005P05Rik	RIKEN cDNA 2310005P05 gene	70805895	67484	NM_026189.2
2310007H09Rik	RIKEN cDNA 2310007H09 gene	72340126	76429	XM_486016.1
2310008M10Rik	RIKEN cDNA 2310008M10 gene	1649	66357	NM_025509
2310009N05Rik	PQ loop repeat containing 1	70927829	66943	NM_025861.1
2310010M24Rik	RIKEN cDNA 2310010M24 gene	73635774	71897	NM_027990.1
2310015N21Rik	raftlin lipid raft linker 1	71920515	76438	NM_181397.1
2310016A09Rik	carboxymethylenebutenolidase-like (Pseudomonas)	1651	69574	NM_181588
2310026E23Rik	RIKEN cDNA 2310026E23 gene	74583139	67621	NM_026279.1
2310028N02Rik	RIKEN cDNA 2310028N02 gene	75774106	66950	NM_025864.2
2310036D04Rik		73512188	69598	XM_488563.1
2310036D22Rik	transmembrane protein 106B	71920509	71900	NM_027992.1
2310042E22Rik	RIKEN cDNA 2310042E22 gene	74357582	66561	NM_025634.1
2310042M24Rik	thioredoxin domain containing 14	71836805	66958	NM_025868.1
2310045A20Rik	RIKEN cDNA 2310045A20 gene	74988657	231238	NM_172710.1
2310046A06Rik	RIKEN cDNA 2310046A06 gene	73931408	69642	XM_146970.3
2310046G15Rik	protease, serine, 23	70634118	76453	NM_029614.2
2310066E14Rik	RIKEN cDNA 2310066E14 gene	75774668	75687	XM_486159.1
2310067E08Rik	endonuclease domain containing 1	71015195	71946	NM_028013.1
2310079N02Rik	RIKEN cDNA 2310079N02 gene	75773704	66566	NM_025636.1
2310079P12Rik	SAP30-like	73907495	50724	XM_203577.3
2410005O16Rik	RIKEN cDNA 2410005O16 gene	75773702	66302	NM_025476.3
2410014A08Rik	RIKEN cDNA 2410014A08 gene	73930854	109154	NM_175403.2
2410018C20Rik	RIKEN cDNA 2410018C20 gene	75773703	67873	NM_026423.2
2410066E13Rik	RIKEN cDNA 2410066E13 gene	71587888	68235	NM_026629.2
2410080H04Rik	multiple EGF-like-domains 11	74357580	214058	NM_172522.1
2510002A14Rik	furry homolog-like (Drosophila)	70431430	72313	NM_028194.1
2510015F01Rik	5'-nucleotidase domain containing 2	73817984	70021	XM_354801.2
2510048O06Rik	proteasome maturation protein	75774685	66537	NM_025624.1
2600003E23Rik	actin filament associated protein 1	74425569	70292	NM_027373.1
2600005N12Rik	ADP-ribosylation factor-like 16	73817933	70317	NM_197995.1
2600013N14Rik	OTU domain containing 6B	83158	72201	NM_152812.1
2610002F03Rik	small nucleolar RNA host gene (non-protein coding) 7	1968	72091	
2610017I09Rik	RIKEN cDNA 2610017I09 gene	77280584	66297	NM_183252.1
2610018G03Rik	RIKEN cDNA 2610018G03 gene	74047829	70415	NM_133729.1
2610019A05Rik	RIKEN cDNA 2610019A05 gene	74819330	72149	NM_028126.1
2610019F03Rik	RIKEN cDNA 2610019F03 gene	74724511	72148	NM_173744.2
2610022G08Rik	phosphatidylinositol glycan anchor biosynthesis, class Y	276271	66459	NM_025574.2
2610024A01Rik	transmembrane protein 163	71670711	72160	XM_129450.4
2610028E06Rik	RIKEN cDNA 2610028E06 gene	71020430	72395	XM_489059.1
2610028F08Rik	R-spondin 2 homolog (Xenopus laevis)	71016632	239405	NM_172815.1
2610031L17Rik	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	67850946	68879	NM_133701.1
2610039E05Rik	spermatogenesis associated 2-like	73817441	78779	NM_030176.2
2610109H07Rik	RIKEN cDNA 2610109H07 gene	74272038	70433	XM_131857.2
2610110G12Rik	RIKEN cDNA 2610110G12 gene	74425517	73242	NM_028476.2
2610206B13Rik	RIKEN cDNA 2610206B13 gene	276273	72486	NM_026047.3
2610318I01Rik	formin binding protein 1-like	70560266	214459	NM_153118.1
2610510B01Rik		31		XM_354972
2610511O17Rik	tetratricopeptide repeat domain 27	74819241	74196	NM_152817.2
2700038N03Rik	RIKEN cDNA 2700038N03 gene	72007932	70240	NM_027356.1

2700045P11Rik	RIKEN cDNA 2700045P11 gene	74363334	72555	XM_148080.2
2700055K07Rik	tubulin polymerization-promoting protein family member 3	70813926	67971	NM_026481.2
2700063A19Rik	tetraspanin 15	70612725	70423	NM_197996.1
2700063G02Rik		2004		
2700084L22Rik	ubiquitin-conjugating enzyme E2T (putative)	276069	67196	NM_026024.1
2810004A10Rik		74958537	69933	NM_027265.1
2810005G07Rik		77340482		
2810031P15Rik	zinc fingerprotein 618	71670712	72701	XM_143826.6
2810036K01Rik	serum response factor binding protein 1	1653		NM_026040
2810401C16Rik	apoptosis-inducing factor, mitochondrion-associated 3	74724774	72168	NM_175178.2
2810405K02Rik	RIKEN cDNA 2810405K02 gene	74047901	66469	NM_025582.2
2810409H07Rik	Obg-like ATPase 1	293038	67059	NM_025942.1
2810417M05Rik	transmembrane protein 178	73992709	68027	NM_026516.1
2810426N06Rik	RIKEN cDNA 2810426N06 gene	1466	67607	NM_023363
2810432L12Rik	RIKEN cDNA 2810432L12 gene	75774671	67063	NM_025944.2
2810439F02Rik	RIKEN cDNA 2810439F02 gene	70743885	72747	NM_028341.1
2810457I06Rik	RIKEN cDNA 2810457I06 gene	74581370	72828	NM_176860.3
2810458H16Rik	protection of telomeres 1B	73925715	72836	XM_355022.2
2900002G04Rik	MAP7 domain containing 2	74272052	78283	XM_136135.3
2900026A02Rik	RIKEN cDNA 2900026A02 gene	71670713	243219	NM_172884.1
2900026H06Rik	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	1655		NM_028392
2900036K24Rik	X-linked lymphocyte-regulated 4C	71670714	72891	NM_183094.1
2900041A09Rik	tubulin polymerization promoting protein	74724775	72948	NM_182839.1
2900042E01Rik	hepatocyte cell adhesion molecule	35	72927	NM_175189
2900045N06Rik	SET domain containing 5	37		NM_028385
2900060P06Rik	LON peptidase N-terminal domain and ring finger 2	74988755	381338	XM_355299.2
2900074C18Rik	tetratricopeptide repeat domain 9B	71249081	73032	XM_355870.2
2900075G08Rik	cornichon homolog 3 (Drosophila)	39		NM_028408
2900093B09Rik	V-set and transmembrane domain containing 2B	72128753	58188	NM_021387.1
2900093B09Rik	V-set and transmembrane domain containing 2B	77869820	58188	NM_021387.1
3000002B06Rik	multiple EGF-like-domains 10	71249082	70417	NM_001001979.1
3010001K23Rik	transmembrane protein 175	356084	72392	NM_028223.2
3100002H09Rik	RIKEN cDNA 3100002H09 gene	77340484	70249	
3100002L24Rik	RIKEN cDNA 3100002L24 gene	293468	66376	XM_355388.2
3110001A13Rik	RIKEN cDNA 3110001A13 gene	71015800	66540	NM_025626.3
3110004L20Rik	RIKEN cDNA 3110004L20 gene	72128754	73102	XM_127295.6
3110006E14Rik	RIKEN cDNA 3110006E14 gene	71249083	76980	XM_127466.5
3110023B02Rik	coiled-coil domain containing 137	1978	67291	NM_152807
3110035E14Rik	RIKEN cDNA 3110035E14 gene	73817427	76982	NM_178399.2
3110047P20Rik	RIKEN cDNA 3110047P20 gene	73771233	319807	XM_132047.4
3110047P20Rik	RIKEN cDNA 3110047P20 gene	73771234	319807	XM_132047.4
3110069A13Rik	Fez family zinc finger 1	72283796	73191	XM_133029.2
3110082D06Rik	RIKEN cDNA 3110082D06 gene	74581400	73235	XM_140020.3
3632451O06Rik	RIKEN cDNA 3632451O06 gene	70928306	67419	NM_026142.1
3732412D22Rik	LIM and calponin homology domains 1	71249084	77569	NM_001001980.1
3830406C13Rik	RIKEN cDNA 3830406C13 gene	276269	218734	NM_146051.1
3830406C13Rik	RIKEN cDNA 3830406C13 gene	77414919	218734	NM_146051.1
4122402O22Rik	sphingomyelin phosphodiesterase 4	75651226	77626	NM_029945.1
4432412L15Rik	RIKEN cDNA 4432412L15 gene	74958547	74337	XM_486140.1



4631422O05Rik	RIKEN cDNA 4631422O05 gene	74363347	78749	XM_489572.1
4631426E05Rik	RIKEN cDNA 4631426E05 gene	75081003	66696	NM_025712.2
4631426J05Rik	RIKEN cDNA 4631426J05 gene	70613978	77590	NM_029935.2
4631427C17Rik	RIKEN cDNA 4631427C17 gene	73929896	74340	NM_021414.3
4632411B12Rik	RIKEN cDNA 4632411B12 gene	74988741	226976	NM_172652.1
4632413K17Rik	amplified in osteosarcoma	876	216440	NM_177614
4732437J24Rik	DnaJ (Hsp40) homolog, subfamily C, member 16	870		NM_172338
4732455O04Rik		75043137		
4832415H08Rik	olfactomedin-like 2B	1980		NM_177068
4832420M10	kinesin family member 26B	71717582	269152	NM_177757.3
4833414E09Rik	RIKEN cDNA 4833414E09 gene	73521828	71633	NM_027845.1
4833420G17Rik	RIKEN cDNA 4833420G17 gene	74047840	67392	NM_026127.3
4833424O15Rik	RIKEN cDNA 4833424O15 gene	70744326	75769	XM_131156.5
4921510J17Rik	RIKEN cDNA 4921510J17 gene	72129254	70894	XM_109772.2
4921511K06Rik	coiled-coil domain containing 136	324214	232664	XM_485735.1
4921517B04Rik	tubulin tyrosine ligase-like family, member 7	72128755	70892	XM_357332.2
4921517L17Rik	RIKEN cDNA 4921517L17 gene	67779872	70873	XM_130609.3
4921531P07Rik	dynein, axonemal, heavy chain 7-like	71670715	207778	XM_138945.3
4930415J21Rik	2-oxoglutarate and iron-dependent oxygenase domain containing 1	74047922	270086	NM_177767.3
4930429A08Rik	S100P binding protein	74819247	74648	XM_131689.5
4930429H24Rik	kelch-like 24 (Drosophila)	1982		NM_029436
4930431J08Rik	zinc finger, DBF-type containing 2	74047400	73884	XM_136658.4
4930431L04Rik	RIKEN cDNA 4930431L04 gene	74750013	270049	NM_175032.1
4930438D12Rik	transmembrane protein 65	73592537	74868	NM_175212.2
4930451C15Rik	RIKEN cDNA 4930451C15 gene	74750011	74685	XM_148428.3
4930473A06Rik	RIKEN cDNA 4930473A06 gene	75080180	74902	XM_194144.4
4930506M07Rik	RIKEN cDNA 4930506M07 gene	322956	71653	NM_175172.2
4930516O21Rik		75043136		
4930544G21Rik	RIKEN cDNA 4930544G21 gene	76085749	77629	NM_172430.1
4930553M18Rik		1317		NM_026541
4930572J05Rik	RIKEN cDNA 4930572J05 gene	72008306	223626	NM_198607.1
4930589M24Rik	RIKEN cDNA 4930589M24 gene	74363348	75906	XM_125625.3
4931406I20Rik	RIKEN cDNA 4931406I20 gene	71924364	66743	NM_025739.2
4931407K02Rik	EF-hand calcium binding domain 3	74819465	77627	NM_029946.3
4931408A02Rik	RIKEN cDNA 4931408A02 gene	1319	70967	XM_354970
4932418E24Rik	RIKEN cDNA 4932418E24 gene	73635776	329366	NM_177841.2
4932418K24Rik	tubulin tyrosine ligase-like family, member 6	74363338	237930	NM_172799.1
4932438H23Rik	RIKEN cDNA 4932438H23 gene	1321	74387	NM_028905
4933403F05Rik	RIKEN cDNA 4933403F05 gene	74819246	108654	NM_153794.2
4933403M22Rik	intermediate filament tail domain containing 1	74425566	74071	NM_028742.1
4933404O19Rik	tetratricopeptide repeat domain 25	74988582	74407	XM_126529.3
4933417K04Rik	coiled-coil domain containing 65	74724776	105833	NM_153518.1
4933417O08Rik	RIKEN cDNA 4933417O08 gene	76097699	71146	XM_203553.4
4933427D14Rik	RIKEN cDNA 4933427D14 gene	74272053	74477	NM_028963.1
4933431N12Rik	TBC1 domain family, member 9	72079987	71310	NM_027758.1
4933440J22Rik	centrosomal protein 72	74988742	74470	NM_028959.1
5031439A09Rik	G protein-coupled receptor 177	72077452	68151	NM_026582.2
5133400D11Rik	Ras association (RalGDS/AF-6) domain family 8	71249739	71323	NM_027760.1
5330421F07Rik	RIKEN cDNA 5330421F07 gene	74641113	78286	Mm.324474.0

5330421K23Rik		75043138		
5330438E18Rik	microtubule associated monooxygenase, calponin and LIM domain containing 2	71249740	320878	NM_177282.2
5330439J01Rik	sine oculis-binding protein homolog (Drosophila)	71920521	109205	NM_175407.2
5430413I02Rik	proline/serine-rich coiled-coil 1	71015388	56742	NM_019976.1
5430433G21Rik	RIKEN cDNA 5430433G21 gene	71249741	319909	XM_283765.2
5730410E15Rik	RIKEN cDNA 5730410E15 gene	70301086	319613	NM_178765.2
5730414C17Rik	hippocampus abundant transcript-like 1	276076	66631	NM_133680.2
5730469D23Rik	ubiquitin-activating enzyme E1-like 2	74819486	231380	NM_172712.2
5730469M10Rik	RIKEN cDNA 5730469M10 gene	70436739	70564	NM_027464.1
5730507A09Rik	RIKEN cDNA 5730507A09 gene	72340182	70638	NM_183087.1
5730578N08Rik	transmembrane protein 41a	70743869	66664	NM_025693.1
5730593N15Rik	notum pectinacylesterase homolog (Drosophila)	73732151	77583	NM_175263.2
5730599I05Rik	centrosomal protein 78	322963	208518	NM_198019.2
5830404H04Rik	RIKEN cDNA 5830404H04 gene	1986	207781	NM_174847
5830445C04Rik	N-6 adenine-specific DNA methyltransferase 1 (putative)	1233		NM_026366
5830461H18Rik	RAS related protein 2a	71016692	76108	NM_029519.2
5830472M02Rik	RIKEN cDNA 5830472M02 gene	74641323	76080	NM_029512.1
6030405A18	RIKEN cDNA 6030405A18 gene	71920518	329641	NM_177854.2
6230405M12Rik		71717144	330336	NM_183310.1
6330403A02Rik	RIKEN cDNA 6330403A02 gene	72340183	381310	XM_484946.1
6330407J23Rik	RIKEN cDNA 6330407J23 gene	1988	67412	NM_026138
6330442E10Rik	RIKEN cDNA 6330442E10 gene	72128773	268567	NM_178745.3
6330500D04Rik	RIKEN cDNA 6330500D04 gene	73635806	193385	XM_484234.1
6330503C03Rik	RIKEN cDNA 6330503C03 gene	72128774	76156	NM_029528.1
6330503K22Rik	RIKEN cDNA 6330503K22 gene	77280311	101565	NM_182995.1
6330505F04Rik	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	75988610	236790	NM_172779.1
6330505N24Rik	RIKEN cDNA 6330505N24 gene	73925717	229474	XM_130991.4
6330509G02Rik	keratin 222	71249742	268481	NM_172946.1
6330514A18Rik	RIKEN cDNA 6330514A18 gene	74988743	216166	NM_183152.1
6330527O06Rik	RIKEN cDNA 6330527O06 gene	70927827	76161	NM_029530.1
6330540D07Rik	transmembrane protein 29	75080656	382245	
6330581L23Rik	zinc finger protein 790	356855	233056	NM_146185.1
6430502M16Rik	RIKEN cDNA 6430502M16 gene	72128747	218440	NM_175455.2
6430514L14Rik	RIKEN cDNA 6430514L14 gene	73732150	76886	XM_135000.4
6430517E21Rik	RIKEN cDNA 6430517E21 gene	71249743	240843	NM_207583.1
6430548M08Rik	RIKEN cDNA 6430548M08 gene	72008118	234797	NM_172286.2
6430573F11Rik	RIKEN cDNA 6430573F11 gene	75651150	319582	NM_176952.3
6430709H04Rik		74750012	319228	XM_484539.1
6530401D17Rik	RIKEN cDNA 6530401D17 gene	45841	76219	NM_029541.1
6530402N02Rik	anterior pharynx defective 1a homolog (C. elegans)	1990		NM_146104
6530406P05Rik	G protein-coupled receptor 165	70560278	76206	XM_135982.2
6530413N01Rik	regulator of G-protein signaling 8	71020445	67792	NM_026380.2
6530418L21Rik	RIKEN cDNA 6530418L21 gene	74819651	109050	NM_175398.3
6620401M08Rik	RIKEN cDNA 6620401M08 gene	73931622	75744	XM_489178.1
6720401G13Rik	RIKEN cDNA 6720401G13 gene	74958576	103012	XM_489349.1
6720456B07Rik	RIKEN cDNA 6720456B07 gene	74988744	101314	NM_133937.1
6820408C15Rik	RIKEN cDNA 6820408C15 gene	74363339	228778	NM_177656.2
7420498E04Rik		75043148		
8030451F13Rik	RIKEN cDNA 8030451F13 gene	71920513	109272	NM_175418.3

8030498B09Rik	RIKEN cDNA 8030498B09 gene	74958606	77547	NM_023867.1
8430415E04Rik	RIKEN cDNA 8430415E04 gene	71249744	74521	NM_028980.1
8430420C20Rik	transmembrane protein 159	76135828	233806	NM_145586.1
8430436L14Rik		73931623	71560	XM_355454.2
8430437G11Rik	transmembrane protein 168	75774112	101118	NM_028990.2
9030224M15Rik	RIKEN cDNA 9030224M15 gene	74581410	327747	NM_177793.2
9030408N13Rik	coiled-coil domain containing 109B	72129249	66815	NM_025779.2
9030409G11Rik	RIKEN cDNA 9030409G11 gene	72007937	71529	NM_144531.2
9030411K21Rik	RIKEN cDNA 9030411K21 gene	51	71557	
9030425E11Rik	RIKEN cDNA 9030425E11 gene	71924353	71566	NM_133733.2
9030603L14Rik	transmembrane protein 35	71587898	67564	NM_026239.2
9030605H24Rik	ATPase, class V, type 10B	73635826	319767	NM_176999.2
9130017A15Rik	PTC7 protein phosphatase homolog (S. cerevisiae)	74881503	320717	NM_177242.3
9130020G22Rik	NIPA-like domain containing 3	70436746	74552	XM_131773.3
9130024F11Rik	RIKEN cDNA 9130024F11 gene	1323	78900	
9130213B05Rik	RIKEN cDNA 9130213B05 gene	75749783	231440	NM_145562.1
9130411I17Rik	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme C (putative)	70301085	67569	NM_026243.2
9130422G05Rik		70634139	66819	NM_025782.2
9130427A09Rik	GRAM domain containing 3	74988591	107022	NM_026240.1
9330128H10Rik	neuropeptide S receptor 1	70560288	319239	NM_175678.2
9330132E09Rik	dermatan sulfate epimerase-like	71249745	319901	XM_283635.3
9330182L06Rik	RIKEN cDNA 9330182L06 gene	75081005	231014	NM_172706.1
9330196J05Rik	arylsulfatase J	71249746	271970	NM_173451.1
9430020E10Rik		75043149		
9430020K01Rik	RIKEN cDNA 9430020K01 gene	75988537	240185	XM_140198.4
9430028L06Rik	RIKEN cDNA 9430028L06 gene	71717154	225617	NM_172629.1
9430063L05Rik	phosphodiesterase 4D interacting protein (myomegalin)	1994		NM_178080
9530058B02Rik	RIKEN cDNA 9530058B02 gene	1996	68241	NM_026633
9530068E07Rik	RIKEN cDNA 9530068E07 gene	74988509	213673	XM_203329.2
9530085C10Rik		75080269		
9530091C08Rik	RIKEN cDNA 9530091C08 gene	71249747	320440	NM_177159.2
9630013P03Rik		77280434		
9630017J07Rik		75080279		
9630020G10Rik	guanine nucleotide binding protein, alpha stimulating, olfactory type	71670716	320338	NM_177137.2
9630031F12Rik	RIKEN cDNA 9630031F12 gene	73636151	58227	NM_021416.2
9630033F20Rik	RIKEN cDNA 9630033F20 gene	71249748	319801	NM_177003.2
9630036J22Rik	patched domain containing 1	71249749	211612	XM_142262.3
9630048M01Rik	zinc finger, matrin type 4	71249750	320158	NM_177086.1
9630050M13Rik	RIKEN cDNA 9630050M13 gene	72283797	269233	XM_194000.4
9830001H06Rik	RIKEN cDNA 9830001H06 gene	77340458	320706	XM_283804.3
9830123M21Rik	RIKEN cDNA 9830123M21 gene	75988547	226438	NM_177642.2
9830166N24Rik		75043150		
9930013L23Rik	RIKEN cDNA 9930013L23 gene	72128775	80982	NM_030728.2
9930021J17Rik	RIKEN cDNA 9930021J17 gene	74363337	229488	NM_172682.1
9930116O05Rik		1998		XM_284500
A030009H04Rik	RIKEN cDNA A030009H04 gene	74750014	80515	NM_020591.1
A030013D21	cDNA sequence BC065085	71924279	219148	NM_177628.3
A130014H13Rik	RIKEN cDNA A130014H13 gene	75041574	319630	Mm.131049.0
A230048G03Rik	HEAT repeat containing 5B	70560265	320473	XM_283480.3

A230057G18Rik	retinal noncoding RNA 2	72340194	330166	XM_489103.1
A230065H16Rik	RIKEN cDNA A230065H16 gene	71250292	380787	XM_354697.1
A230083H22Rik	RIKEN cDNA A230083H22 gene	74363335	353211	NM_181348.2
A230083H22Rik	RIKEN cDNA A230083H22 gene	77874616		XM_990995.1
A230097P14Rik		75042236		
A230109K23Rik		55		
A330019N05Rik	retinaldehyde binding protein 1-like 2	71924374	215890	NM_175448.2
A330043P19Rik		75144634		
A330066M24Rik		71670719	320357	XM_355247.2
A330102H22Rik	prune homolog 2 (Drosophila)	57	77754	XM_355150
A430031N04	RIKEN cDNA 1600021P15 gene	71924290	239796	NM_177718.2
A430041E17Rik		75042237		
A430091O22Rik	ribonucleoprotein, PTB-binding 2	72128776	242570	NM_183024.1
A430107P09Rik	RIKEN cDNA A430107P09 gene	71670720	320898	NM_177288.2
A4galt	alpha 1,4-galactosyltransferase	71717165	239559	NM_001004150.1
A530057D15Rik		75042238		
A530079E22Rik	RIKEN cDNA A530079E22 gene	71250305	319977	NM_177048.2
A530082C11Rik	RIKEN cDNA A530082C11 gene	74881514	320541	NM_177186.3
A530088H08Rik	RIKEN cDNA A530088H08 gene	72283798	193003	NM_178656.2
A630029G22Rik	solute carrier family 2 (facilitated glucose transporter), member 13	74958626	239606	XM_139529.4
A630047E20Rik	RIKEN cDNA A630047E20 gene	77278971	271981	NM_173032.1
A630094N22Rik		75144644		
A730030A06	-	73930833	328235	XM_488677.1
A730041O15Rik	ORAI calcium release-activated calcium modulator 2	73925718	269717	NM_178751.2
A730073J23Rik		75042239		
A730081H18Rik		77280438		
A730096I18Rik		75144645		
A830006N08Rik	ankyrin repeat domain 43	71250306	237761	NM_183173.1
A830018L16Rik	RIKEN cDNA A830018L16 gene	73818758	320492	NM_177173.3
A830039N20Rik	RIKEN cDNA A830039N20 gene	72340208	268723	NM_175545.3
A830041P22Rik	transmembrane protein 91	75651161	320208	NM_177102.2
A830073O21Rik	RIKEN cDNA A830073O21 gene	74819036	320262	NM_177118.2
A930001K06Rik		75042240		
A930001M12Rik	RIKEN cDNA A930001M12 gene	73636150	320500	NM_177175.2
A930009E05Rik	RIKEN cDNA A930009E05 gene	72340221	77796	XM_489135.1
A930009N24	-	74047747	329876	XM_489052.1
A930017N06Rik	leucine rich repeat and fibronectin type III, extracellular 1	71587930	243312	NM_175522.2
A930021G21Rik	ankyrin repeat domain 33	2006		NM_144790
A930027K05Rik	phospholipase C, eta 2	74724786	269615	NM_175556.2
A930038C07Rik	RIKEN cDNA A930038C07 gene	72080134	68169	NM_172399.1
A930041I02Rik	RIKEN cDNA A930041I02 gene	74581420	320271	NM_178778.2
AA415817	pyridoxal-dependent decarboxylase domain containing 1	355891	94184	NM_053181.1
AA517853	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	275872	353190	NM_153799.1
AA536743	RELT-like 1	72007746	100532	NM_145923.1
AA536743	RELT-like 1	2008	100532	NM_145923
AA691260	low density lipoprotein receptor adaptor protein 1	2010		NM_145554
Aacs	acetoacetyl-CoA synthetase	74988454	78894	NM_030210.1
Aadacl1	arylacetamide deacetylase-like 1	74881744	320024	NM_178772.2
Aars	alanyl-tRNA synthetase	74641317	234734	NM_146217.3

AB114826	beta-1,4-N-acetyl-galactosaminyl transferase 3	73636090	330406	NM_198884.1
Abat	4-aminobutyrate aminotransferase	72079931	268860	NM_172961.2
Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	74881353	56199	NM_019552.1
Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	67881549	74104	NM_023732.2
Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	75749413	74104	NM_023732.2
Abcd1	ATP-binding cassette, sub-family D (ALD), member 1	356086	11666	NM_007435.1
Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	70616004	26874	NM_011994.1
Abhd3	abhydrolase domain containing 3	70744514	106861	NM_134130.1
Abhd6	abhydrolase domain containing 6	74047923	66082	NM_025341.2
Abhd8	abhydrolase domain containing 8	2012	64296	NM_022419
Ablim2	actin-binding LIM protein 2	73636039	231148	NM_177678.3
Ablim3	actin binding LIM protein family, member 3	73992943	319713	NM_198649.1
Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	1659	80283	NM_030251
Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	71924375	52538	NM_177470.2
Acacb	acetyl-Coenzyme A carboxylase beta	74881515	100705	NM_133904.1
Acadl	acyl-Coenzyme A dehydrogenase, long-chain	72081416	11363	NM_007381.2
Acadvl	acyl-Coenzyme A dehydrogenase, very long chain	227161	11370	NM_017366.1
Acat1	acetyl-Coenzyme A acetyltransferase 1	71836840	110446	NM_144784.2
Acat2	acetyl-Coenzyme A acetyltransferase 2	655500	110460	NM_009338.1
Acat2	acetyl-Coenzyme A acetyltransferase 2	77869798	110460	NM_009338.1
Accn1	amiloride-sensitive cation channel 1, neuronal (degenerin)	73930838	11418	NM_007384.1
Accn4	amiloride-sensitive cation channel 4, pituitary	71924089	241118	NM_183022.1
Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	73512499	11421	NM_009598.1
Ache	acetylcholinesterase	70301082	11423	NM_009599.2
Aco1	aconitase 1	76135819	11428	NM_007386.1
Acpl2	acid phosphatase-like 2	293473	235534	NM_153420.1
Acsl3	acyl-CoA synthetase long-chain family member 3	75042266	74205	XM_129894.4
Acsl5	acyl-CoA synthetase long-chain family member 5	73931635	433256	XM_484816.1
Acsl6	acyl-CoA synthetase long-chain family member 6	71836810	216739	NM_144823.1
Acta1	actin, alpha 1, skeletal muscle	60	11459	NM_009606
Actb	actin, beta, cytoplasmic	74881516	11461	NM_007393.1
Actc1	actin, alpha, cardiac	62	11464	NM_009608
Actr10	ARP10 actin-related protein 10 homolog (S. cerevisiae)	64	56444	NM_019785
Actr1a	ARP1 actin-related protein 1 homolog A (yeast)	321206	54130	NM_016860.1
Actr2	ARP2 actin-related protein 2 homolog (yeast)	67	66713	NM_146243
Acvr1c	activin A receptor, type IC	71250307	269275	XM_194020.4
Acvr1l	activin A receptor, type II-like 1	2014	11482	NM_009612
Acyp1	acylphosphatase 1, erythrocyte (common) type	74988760	66204	NM_025421.1
Acyp2	acylphosphatase 2, muscle type	73930820	75572	NM_029344.1
Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)	74272054	11492	NM_009616.2
Adam33	a disintegrin and metallopeptidase domain 33	75147767	110751	NM_033615.1
Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	69	11504	NM_009621
Adamts15	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 15	77332098	235130	XM_134720.6
Adamts16	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 16	276267	271127	NM_172053.1
Adamts18	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 18	75651128	208936	NM_172466.1
Adamts19	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19	73635973	240322	NM_175506.2
Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2	71924385	216725	NM_175643.1
Adamts4	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4	71836845	240913	NM_172845.1
Adamts8	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8	73925719	30806	NM_013906.1

Adamts8	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8	77869834	30806	NM_013906.1
Adamts12	ADAMTS-like 2	74881352	77794	XM_130065.5
Adamts13	ADAMTS-like 3	73925720	269959	XM_194370.4
Adarb1	adenosine deaminase, RNA-specific, B1	73636040	110532	NM_130895.1
Adarb2	adenosine deaminase, RNA-specific, B2	73925721	94191	NM_052977.2
Adck4	aarF domain containing kinase 4	70743880	76889	NM_133770.1
Adcy1	adenylate cyclase 1	71	432530	
Adcy2	adenylate cyclase 2	73	210044	NM_153534
Adcy3	adenylate cyclase 3	75	104111	NM_138305
Adcy4	adenylate cyclase 4	73512495	104110	NM_080435.1
Adcy5	adenylate cyclase 5	79	224129	XM_358801
Adcy6	adenylate cyclase 6	81	11512	NM_007405
Adcy7	adenylate cyclase 7	2017	11513	NM_007406
Adcy7	adenylate cyclase 7	77866898	11513	NM_007406.1
Adcy8	adenylate cyclase 8	77280540	11514	NM_009623.1
Adcy9	adenylate cyclase 9	83	11515	NM_009624
Adcyap1	adenylate cyclase activating polypeptide 1	74511882	11516	NM_009625.2
Adcyap1r1	adenylate cyclase activating polypeptide 1 receptor 1	74988667	11517	NM_007407.2
Adipor1	adiponectin receptor 1	61210	72674	NM_028320.2
Adk	adenosine kinase	70928196	11534	NM_134079.1
Adm	adrenomedullin	74819251	11535	NM_009627.1
Adra1a	adrenergic receptor, alpha 1a	75042247	11549	NM_013461.2
Adra1d	adrenergic receptor, alpha 1d	72119628	11550	NM_013460.1
Adra2a	adrenergic receptor, alpha 2a	73615550	11551	NM_007417.1
Adra2b	adrenergic receptor, alpha 2b	74724532	11552	NM_009633.2
Adrb1	adrenergic receptor, beta 1	77340494	11554	NM_007419.1
Adrbk2	adrenergic receptor kinase, beta 2	74724787	320129	NM_177078.2
Adrm1	adhesion regulating molecule 1	2019	56436	NM_019822
Adssl1	adenylosuccinate synthetase like 1	72104185	11565	NM_007421.1
AF529169	cDNA sequence AF529169	73636152	209743	NM_153509.1
Agc1	aggreCAN	72128777	11595	NM_007424.1
Agc1	aggreCAN	77869840	11595	NM_007424.1
Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	85	28169	NM_053014
Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	73718048	68262	NM_026644.1
Agps	alkylglycerone phosphate synthase	74819325	228061	NM_172666.2
Agrn	agrin	73925722	11603	NM_021604.2
Agrp	agouti related protein	72283799	11604	NM_007427.2
Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	87	11606	NM_007428
Agtr1	angiotensin receptor-like 1	2021	23796	NM_177322
Agtr1b	angiotensin II receptor, type 1b	74724627	11608	NM_175086.2
Agtrl1	angiotensin receptor-like 1	1661		NM_011784
Agxt2l1	alanine-glyoxylate aminotransferase 2-like 1	75079777	71760	NM_027907.1
AI326477	serine/threonine/tyrosine kinase 1	71250308	243659	NM_172891.1
AI413414	CREB regulated transcription coactivator 1	71250309	382056	NM_001004062.1
AI415282	pyridoxine 5'-phosphate oxidase	70743879	103711	NM_134021.1
AI415330	adhesion molecule with Ig like domain 2	71250310	105827	NM_178114.2
AI427515	expressed sequence AI427515	75650860	270097	NM_173016.2
AI450948	AHNAK nucleoprotein 2	71250311	382643	XM_356602.2
AI481750	cold shock domain containing C2, RNA binding	70634234	105859	NM_145473.1

AI593442	expressed sequence AI593442	71250312	330941	NM_177907.2
AI606473	expressed sequence AI606473	1468	99686	
AI649392	clarin 3	2023		NM_178669
AI836003	expressed sequence AI836003	71250313	239650	NM_177716.1
AI839550	alkB, alkylation repair homolog 6 (E. coli)	323594	233065	NM_198027.2
AI839562	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	89		NM_019914
AI839735	transmembrane protein 179	76097701	104885	NM_178915.2
AI841794	leucine-rich repeats and transmembrane domains 2	74819475	211187	NM_172492.2
AI848100	expressed sequence AI848100	71250314	226551	XM_484932.1
AI851790	expressed sequence AI851790	73636033	268354	NM_182807.1
AI852640		74958645	380744	XM_354658.2
AI854408	vezatin, adherens junctions transmembrane protein	74819329	215008	NM_172538.2
AI987712		72340223	105935	NM_178921.2
Aif1	allograft inflammatory factor 1	75080249	11629	NM_019467.2
Aim1	absent in melanoma 1	71250315	11630	NM_172393.1
Aip1	aryl hydrocarbon receptor-interacting protein-like 1	67855411	114230	NM_053245.1
Aire	autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy)	1327	11634	NM_009646
Ak1	adenylate kinase 1	83164	11636	NM_021515.1
Ak1	adenylate kinase 1	77414110	11636	NM_021515.1
Ak31	adenylate kinase 3 alpha-like 1	74641312	11639	NM_009647.2
Ak4	adenylate kinase 3 alpha-like 1	77		NM_009647
Akap12	A kinase (PRKA) anchor protein (gravin) 12	72128778	83397	NM_031185.1
Akap2	A kinase (PRKA) anchor protein 2	1448	11641	NM_009649
Akap8	A kinase (PRKA) anchor protein 8	91	56399	NM_019774
Akr1b3	aldo-keto reductase family 1, member B3 (aldose reductase)	70813922	11677	NM_009658.2
Akr1c18	aldo-keto reductase family 1, member C18	74425542	105349	NM_134066.1
Akr1e1	aldo-keto reductase family 1, member E1	356093	56043	NM_018859.1
AL024069	RIKEN cDNA 5033414K04 gene	73635974	98496	NM_001003948.1
AL033314	staphylococcal nuclease and tudor domain containing 1	355881	56463	NM_019776.1
AL033314	staphylococcal nuclease and tudor domain containing 1	77869128	56463	NM_019776.1
Alcam	activated leukocyte cell adhesion molecule	70928271	11658	NM_009655.1
Aldh1a1	aldehyde dehydrogenase family 1, subfamily A1	72103809	11668	NM_013467.1
Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	2025	19378	NM_009022
Aldh2	aldehyde dehydrogenase 2, mitochondrial	74819240	11669	NM_009656.1
Aldh5a1	aldehyde dehydrogenase family 5, subfamily A1	77925007	214579	NM_172532.1
Aldob	aldolase 2, B isoform	77371801	230163	NM_144903.2
Aldoc	aldolase 3, C isoform	72007559	11676	XM_126120.6
Alg1	asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase)	70616016	208211	NM_145362.1
Alg14	asparagine-linked glycosylation 14 homolog (yeast)	75081004	66789	NM_024178.1
Alg2	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	73931383	56737	NM_019998.2
Alg5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	75774105	66248	NM_025442.1
Alk	anaplastic lymphoma kinase	77371829	11682	NM_007439.1
Alkbh6	alkB, alkylation repair homolog 6 (E. coli)	77414882	233065	NM_198027.2
Allc	allantoicase	74581421	94041	NM_053156.1
Alox12b	arachidonate 12-lipoxygenase, 12R type	72128779	11686	NM_009659.1
Alox15b	arachidonate 8-lipoxygenase	73718055	11688	NM_009661.2
Alpk2	alpha-kinase 2	74988275	225638	XM_128981.3
Amot	angiomin	74425553	27494	NM_153319.1
Amotl1	angiomin-like 1	75038463	75723	XM_134711.4

Ampd3	AMP deaminase 3	77371807	11717	NM_009667.1
Amph	amphiphysin	72340233	218038	NM_175007.1
Ank	progressive ankylosis	75934916	11732	NM_020332.2
Ank1	ankyrin 1, erythroid	70560276	11733	NM_031158.1
Ank2	ankyrin 2, brain	71924087	109676	NM_178655.2
Ank3	ankyrin 3, epithelial	74047925	11735	NM_009670.2
Ankrd10	ankyrin repeat domain 10	2027	102334	NM_133971
Ankrd25	ankyrin repeat domain 25	1160	235041	NM_145611
Ankrd38	ankyrin repeat domain 38	76085741	242553	NM_172872.2
Ankrd6	ankyrin repeat domain 6	71247671	140577	NM_080471.2
Anln	anillin, actin binding protein (scraps homolog, Drosophila)	33	68743	NM_028390
Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	94	11737	NM_009672
Anxa1	annexin A1	70813897	16952	NM_010730.1
Anxa11	annexin A11	2029	11744	NM_013469
Anxa2	annexin A2	70928384	12306	NM_007585.2
Anxa3	annexin A3	72283800	11745	NM_013470.1
Anxa4	annexin A4	70436730	11746	NM_013471.1
Anxa5	annexin A5	1154	11747	NM_009673
Anxa6	annexin A6	77332100	11749	NM_013472.2
Aox1	aldehyde oxidase 1	74425525	11761	NM_009676.1
Ap1b1	adaptor protein complex AP-1, beta 1 subunit	356859	11764	NM_007454.1
Ap1b1	adaptor protein complex AP-1, beta 1 subunit	77869778	11764	NM_007454.1
Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	74819476	11772	NM_007459.2
Ap2b1	adaptor-related protein complex 2, beta 1 subunit	96	71770	NM_027915
Ap2m1	adaptor protein complex AP-2, mu1	100	11773	NM_009679
Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	71836889	232910	NM_198613.1
Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	73512483	11777	NM_009681.2
Apba1	amyloid beta (A4) precursor protein binding, family A, member 1	74658000	319924	NM_177034.2
Apba1	amyloid beta (A4) precursor protein binding, family A, member 1	77869854	319924	NM_177034.2
Apba2	amyloid beta (A4) precursor protein-binding, family A, member 2	2031	11784	NM_007461
Apba2bp	amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein	73771235	56846	NM_021546.1
Apba2bp	amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein	73771236	56846	NM_021546.1
Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	2033	11785	NM_009685
Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	72128788	11787	NM_009686.1
Apbb3	amyloid beta (A4) precursor protein-binding, family B, member 3	77371771	225372	NM_146085.1
Apc	adenomatosis polyposis coli	74881517	11789	NM_007462.1
Apln	apelin	67850953	30878	NM_013912.2
Apoe	apolipoprotein E	77278969	11816	NM_009696.2
Apol2	apolipoprotein L 8	74581422	239552	XM_139463.3
App	amyloid beta (A4) precursor protein	106	11820	NM_007471
Aqp2	aquaporin 2	121093	11827	NM_009699.2
Aqp3	aquaporin 3	293692	11828	NM_016689.1
Aqp4	aquaporin 4	108	11829	NM_009700
Aqp9	aquaporin 9	2037	64008	NM_022026
Ar	androgen receptor	2039	11835	NM_013476
Arbp	acidic ribosomal phosphoprotein P0	74047927	11837	NM_007475.2
Arc	activity regulated cytoskeletal-associated protein	74273120	11838	NM_018790.1
Arf1	ADP-ribosylation factor 1	199390	11840	NM_007476.2
Arf1	ADP-ribosylation factor 1	77414125	11840	NM_007476.2



Arf3	ADP-ribosylation factor 3	655120	11842	NM_007478.2
Arf3	ADP-ribosylation factor 3	110	11842	NM_007478
Arf4l	ADP-ribosylation factor-like 4D	73817442	80981	NM_031160.1
Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	162	99371	XM_130646
Arf4l	ADP-ribosylation factor-like 4D	73817927	66182	NM_025404.1
Arfrp2	ADP-ribosylation factor-like 15	74363341	218639	NM_172595.1
Arg2	arginase type II	70928338	11847	NM_009705.1
Arhgap12	Rho GTPase activating protein 12	71836846	75415	NM_029277.1
Arhgap17	Rho GTPase activating protein 17	1413	70497	NM_144529
Arhgap25	Rho GTPase activating protein 25	72128789	232201	NM_175476.2
Arhgap26	Rho GTPase activating protein 26	75080997	71302	NM_175164.2
Arhgap27	Rho GTPase activating protein 27	75774664	544817	NM_133715.1
Arhgap5	Rho GTPase activating protein 5	113	11855	NM_009706
Arhgdia	Rho GDP dissociation inhibitor (GDI) alpha	75774677	192662	NM_133796.3
Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	2041	14570	NM_008113
Arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	77280329	234094	NM_172751.1
Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2	2043	16800	NM_008487
Arhgef5	Rho guanine nucleotide exchange factor (GEF) 5	74881537	54324	XM_133067.4
Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	74881547	73341	NM_152801.1
Arid1b	AT rich interactive domain 1B (Swi1 like)	982	239985	XM_139711
Arid5a	AT rich interactive domain 5A (Mrf1 like)	75042267	214855	NM_145996.2
Arl10a	ADP-ribosylation factor-like 10	74658019	56795	NM_019968.1
Arl2	ADP-ribosylation factor-like 2	74819344	56327	NM_019722.3
Arl3	ADP-ribosylation factor-like 3	75043143	56350	NM_019718.2
Arl5	ADP-ribosylation factor-like 5A	74274688	75423	NM_182994.1
Arl6ip5	ADP-ribosylation factor-like 6 interacting protein 5	75651232	65106	NM_022992.1
Arl7	ADP-ribosylation factor-like 4C	74988455	320982	NM_177305.2
Arnt2	aryl hydrocarbon receptor nuclear translocator 2	71358590	11864	NM_007488.2
Arntl	aryl hydrocarbon receptor nuclear translocator-like	2045	11865	NM_007489
Arpc1a	actin related protein 2/3 complex, subunit 1A	77280335	56443	NM_019767.1
Arrdc3	arrestin domain containing 3	77280426	105171	NM_178917.2
Arsa	arylsulfatase A	75749415	11883	NM_009713.1
Arx	aristaless related homeobox gene (Drosophila)	118	11878	NM_007492
Asb11	ankyrin repeat and SOCS box-containing protein 11	71836891	68854	NM_026853.1
Asb13	ankyrin repeat and SOCS box-containing protein 13	72081558	142688	NM_080857.1
Asb4	ankyrin repeat and SOCS box-containing protein 4	71358591	65255	NM_023048.4
Asb6	ankyrin repeat and SOCS box-containing protein 6	1599	72323	NM_133346
Asb8	ankyrin repeat and SOCS box-containing protein 8	276276	78541	NM_030121.2
Asb8	ankyrin repeat and SOCS box-containing protein 8	77414921	78541	NM_030121.2
Ascl1	achaete-scute complex homolog-like 1 (Drosophila)	73817423	17172	NM_008553.2
Ascl2	achaete-scute complex homolog-like 2 (Drosophila)	1156	17173	NM_008554
Asgr1	asialoglycoprotein receptor 1	2047	11889	NM_009714
Asns	asparagine synthetase	74047788	27053	NM_012055.1
Aspa	aspartoacylase (aminoacylase) 2	77371803	11484	NM_023113.3
Astn2	astrotactin 2	74047748	56079	NM_019514.2
Atbf1	zinc finger homeobox 3	74641308	11906	NM_007496.1
Atf3	activating transcription factor 3	70814344	11910	NM_007498.2
Atg12l	autophagy-related 12 (yeast)	74881536	67526	NM_026217.1
Atg3l	autophagy-related 3 (yeast)	74988519	67841	NM_026402.1

Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	72077466	108147	NM_026195.1
Atm	ataxia telangiectasia mutated homolog (human)	1329	11920	NM_007499
Atp10a	ATPase, class V, type 10A	72128790	11982	NM_009728.1
Atp11b	ATPase, class VI, type 11B	70744324	76295	XM_358349.2
Atp11c	Atpase, class VI, type 11C	74750077	320940	NM_001001798.1
Atp11c	Atpase, class VI, type 11C	74047410	320940	NM_001001798.1
Atp13a5	ATPase type 13A5	74658053	268878	NM_175650.2
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	71836844	11928	NM_144900.1
Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	74881263	232975	NM_144921.1
Atp1a4	ATPase, Na+/K+ transporting, alpha 4 polypeptide	74881548	27222	XM_355283.2
Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	74819255	11932	NM_013415.2
Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	74881549	11938	NM_009722.1
Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	77280449	67972	XM_483944.1
Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	1579	11946	NM_007505
Atp5h	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	77371785	71679	NM_027862.1
Atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	124	11957	NM_016755
Atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	323589	68055	NM_026536.1
Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	126	11975	NM_016920
Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	357094	21871	NM_011596.1
Atp6v0b	ATPase, H+ transporting, lysosomal V0 subunit B	293682	114143	NM_033617.1
Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	74881559	11984	NM_009729.1
Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	74641315	11964	NM_007508.2
Atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	129	11966	NM_007509
Atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2	74881265	68775	NM_133699.1
Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	74047915	73834	NM_023721.1
Atp6v1e1	VATPase, H+ transporting, lysosomal V1 subunit E1	655501	11973	NM_007510.2
Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	74881560	11980	NM_009727.1
Atp8a2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	73925723	50769	NM_015803.1
Atp9b	ATPase, class II, type 9B	74272466	50771	NM_015805.2
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	77280419	230649	NM_181040.2
Atpif1	ATPase inhibitory factor 1	75774682	11983	NM_007512.2
Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	74881733	22589	NM_009530.1
AU040377	EGF-like, fibronectin type III and laminin G domains	74047441	268780	NM_178748.3
AU040576	transmembrane protein 16A	1472		NM_178642
AV216087	DEP domain containing 7	70743883	211896	NM_144804.1
AV344025		73635975	106755	NM_178927.2
Avil	advillin	72340234	11567	NM_009635.2
Avp	arginine vasopressin	131	11998	NM_009732
Avpr1a	arginine vasopressin receptor 1A	74641316	54140	NM_016847.2
AW046396		72340236	329173	NM_177836.2
AW049765	signal transducing adaptor family member 2	73512501	106766	NM_145934.1
AW125753	expressed sequence AW125753	70927811	105005	NM_029007.2
AW146242	expressed sequence AW146242	70928373	232023	NM_146168.1
AW210570	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	2051		NM_025296
AW456874	protein tyrosine phosphatase domain containing 1	72472738	218232	NM_207232.1
AW538212		1665		XM_358354
Axin1	axin 1	2053	12005	NM_009733
Axin2	axin2	74819487	12006	NM_015732.3
Azin1	antizyme inhibitor 1	74047917	54375	NM_018745.2

B130008G09Rik		75042241		
B130017P16Rik	transmembrane protein 108	71358589	81907	NM_178638.2
B130052G07Rik	vasohibin 2	1667	226841	NM_144879
B230114H05Rik		75043139		
B230114J08Rik	transmembrane protein 50B	133		NM_030018
B230120H23Rik	RIKEN cDNA B230120H23 gene	2049	65964	NM_023057
B230206N24Rik	proline-rich transmembrane protein 3	72081547	210673	NM_172487.1
B230209C24Rik	RIKEN cDNA B230209C24 gene	77280313	320705	NM_177235.3
B230215L15Rik	RIKEN cDNA B230215L15 gene	74658020	320478	NM_177170.2
B230218L05Rik	RIKEN cDNA B230218L05 gene	72472747	330998	NM_207260.1
B230220E17Rik	cadherin 18	74658022	320865	XM_484451.1
B230308C24Rik		75042242		
B230312C02Rik	RIKEN cDNA B230312C02 gene	74363336	320485	XM_488981.1
B230317C12Rik	RIKEN cDNA B230317C12 gene	73635786	56279	NM_019833.1
B230343H07Rik	NEL-like 1 (chicken)	74357567	338352	NM_177413.2
B230362M20Rik		77340460	320835	NM_177273.1
B230373P09Rik		73520818	218878	NM_177336.2
B230382K22Rik	transmembrane protein 74	74881364	239408	NM_175502.2
B230399E16Rik	RIKEN cDNA B230399E16 gene	73636086	240479	NM_173770.2
B2m	beta-2 microglobulin	71924291	12010	NM_009735.2
B3bp	Bcl3 binding protein	74363354	333789	NM_001024917.1
B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	71064081	26878	NM_020025.2
B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	1158	93961	NM_033149
B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	77280578	93961	NM_033149.2
B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	73818755	76898	NM_029792.1
B3gat2	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S)	74658033	280645	NM_172124.2
B3gnt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	77332102	53625	NM_175383.1
B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	75988600	53625	NM_016888.4
B3gnt5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	73992711	108105	NM_054052.2
B430110C06Rik		75043140		
B430201A12Rik	RIKEN cDNA B430201A12 gene	73520819	329739	XM_283903.2
B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	71063735	14595	NM_022305.2
B4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	357099	57370	NM_020579.1
B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	73635976	56336	NM_019835.1
B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	2055	56386	NM_019737
B530004C07Rik		75042243		
B630019K06Rik	RIKEN cDNA B630019K06 gene	74881160	102941	NM_175327.2
B830021E24Rik	SID1 transmembrane family, member 1	71587812	320007	NM_198034.2
B830028B13Rik	RIKEN cDNA B830028B13 gene	75042244	627214	
B830028H17Rik		75042245		
B830045N13Rik	RIKEN cDNA B830045N13 gene	70927812	215378	NM_153539.1
B930010G24Rik		75042246		
B930011P16Rik	RIKEN cDNA B930011P16 gene	73520981	403186	NM_207282.1
B930013M22Rik	ras responsive element binding protein 1	72340134	68750	XM_127279.5
B930052A04Rik	immunoglobulin superfamily containing leucine-rich repeat 2	142		NM_177193
B930076A02	transmembrane protein 145	74511987	330485	NM_183311.1
Baalc	brain and acute leukemia, cytoplasmic	73520964	118452	NM_080640.3
Bace1	beta-site APP cleaving enzyme 1	73520965	23821	NM_011792.3
Bace2	beta-site APP-cleaving enzyme 2	143	56175	NM_019517

Bach	acyl-CoA thioesterase 7	145		NM_133348
Bad	Bcl-associated death promoter	74881790	12015	NM_007522.1
Bag1	Bcl2-associated athanogene 1	75043147	12017	NM_009736.1
Bag2	Bcl2-associated athanogene 2	70634296	213539	NM_145392.1
Bai3	brain-specific angiogenesis inhibitor 3	71247597	210933	NM_175642.2
Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	73520966	108100	NM_130862.1
Banp	Btg3 associated nuclear protein	67755432	53325	NM_016812.1
Bap1	Brca1 associated protein 1	74881827	104416	NM_027088.1
Barx2	BarH-like homeobox 2	2057	12023	NM_013800
Baz1a	bromodomain adjacent to zinc finger domain 1A	73635977	217578	XM_484142.1
BB146404	expressed sequence BB146404	70928307	103511	NM_178908.2
BC002236	ubiquitin-like domain containing CTD phosphatase 1	70634406	79560	NM_024475.2
BC004044	cDNA sequence BC004044	654929	80752	NM_030565.5
BC005471	zinc finger protein 810	356856	235050	NM_145612.1
BC005537	cDNA sequence BC005537	321201	79555	NM_024473.2
BC005561	cDNA sequence BC005561	74988761	243171	XM_144450.4
BC005624	cDNA sequence BC005624	67936203	227707	NM_144885.1
BC005752	ATP binding domain 3	70927830	233189	NM_145582.1
BC005764	cDNA sequence BC005764	73925724	216152	NM_181681.1
BC008103	misato homolog 1 (Drosophila)	1379		NM_144898
BC011467	spinstar homolog 2 (Drosophila)	73512500	216892	XM_484044.1
BC016235	hexokinase domain containing 1	70634299	216019	NM_145419.1
BC017634	CaM kinase-like vesicle-associated	70743867	235604	NM_145621.1
BC018242	cDNA sequence BC018242	71836832	235044	NM_144935.1
BC022146	echinoderm microtubule associated protein like 3	71015805	225898	NM_144872.1
BC022623	cDNA sequence BC022623	72472748	224093	NM_177632.2
BC022765	ATPase family, AAA domain containing 4	74819231	217138	NM_146026.1
BC023818	transmembrane and tetratricopeptide repeat containing 1	73636154	387314	NM_198967.1
BC023892	cDNA sequence BC023892	73520967	212943	XM_135029.4
BC025816	cDNA sequence BC025816	2061	234796	NM_146219
BC025816	cDNA sequence BC025816	77371861	234796	NM_146219.1
BC027127	V-set and transmembrane domain containing 2A	71836843	211739	NM_145967.1
BC028663	cDNA sequence BC028663	74750064	234365	XM_134244.2
BC029169	cDNA sequence BC029169	70744517	208659	NM_153782.1
BC030477	WSC domain containing 1	71920517	216881	NM_177618.4
BC031181	cDNA sequence BC031181	73718052	407819	NM_001001181.2
BC031353	cDNA sequence BC031353	77371767	235493	NM_153584.1
BC032203	cDNA sequence BC032203	2349	210982	XM_140041
BC032203	cDNA sequence BC032203	77867708	210982	XM_140041.4
BC032265	cDNA sequence BC032265	74819239	238024	NM_181420.2
BC033915	cDNA sequence BC033915	74881867	70661	NM_027498.2
BC034054	sterile alpha motif domain containing 14	73930839	217125	NM_146025.1
BC034068	N-acetyltransferase 8-like	74958656	269642	NM_001001985.1
BC034076	hemicentin 2	71836848	227712	NM_177649.3
BC035295	cDNA sequence BC035295	74047914	207785	NM_153407.1
BC037006	WW, C2 and coiled-coil domain containing 1	71020388	211652	XM_109956.5
BC040774	complement component 1, q subcomponent-like 2	71587929	226359	NM_207233.1
BC049816	glycosyltransferase 8 domain containing 4	73931405	232313	NM_198612.1
BC051227	cDNA sequence BC051227	74988601	234384	NM_183170.1

BC052055	cDNA sequence BC052055	71587835	328643	NM_182636.1
BC052328	cDNA sequence BC052328	74819326	223433	NM_198301.1
BC053073	relaxin family peptide receptor 3	71358555	239336	NM_178717.2
BC053994		77340462	381383	XM_355347.2
BC054438	cDNA sequence BC054438	73769320	407831	NM_001001183.1
BC057079	cDNA sequence BC057079	74881879	230393	XM_283973.3
BC059842	cDNA sequence BC059842	1446	230676	NM_198170
BC060632	cDNA sequence BC060632	77332715	244654	NM_198625.1
BC061928	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	70436744	241919	NM_172861.2
BC062109	cDNA sequence BC062109	77340478	231503	NM_182841.1
BC064033	cDNA sequence BC064033	72283801	208164	NM_173375.1
BC067047	cDNA sequence BC067047	73925725	277360	XM_485102.1
Bcan	brevican	154	12032	NM_007529
Bcap29	B-cell receptor-associated protein 29	104826	12033	NM_007530.2
Bcar3	breast cancer anti-estrogen resistance 3	77371769	29815	NM_013867.1
Bcas1	breast carcinoma amplified sequence 1	77371831	76960	NM_029815.1
Bcat1	branched chain aminotransferase 1, cytosolic	71016665	12035	NM_007532.1
Bche	butyrylcholinesterase	74881889	12038	NM_009738.1
Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide	71836890	12040	NM_199195.1
Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	71836837	14025	NM_016707.1
Bcl2l11	BCL2-like 11 (apoptosis facilitator)	74658243	12125	NM_009754.2
Bcl2l12	BCL2-like 12 (proline rich)	71064289	75736	NM_029410.1
Bcl6	B-cell leukemia/lymphoma 6	75651139	12053	NM_009744.2
Bcl7b	B-cell CLL/lymphoma 7B	1601	12054	NM_009745
Bcl7c	B-cell CLL/lymphoma 7C	70743235	12055	NM_009746.2
Bdnf	brain derived neurotrophic factor	71015808	12064	NM_007540.3
Bdnf	brain derived neurotrophic factor	157	12064	NM_007540
Bhlhb2	basic helix-loop-helix domain containing, class B2	356488	20893	NM_011498.2
Bhlhb3	basic helix-loop-helix domain containing, class B3	73521802	79362	NM_024469.1
Bhlhb5	basic helix-loop-helix domain containing, class B5	1162	59058	NM_021560
Bhlhb9	basic helix-loop-helix domain containing, class B9	74274689	70237	NM_198161.1
Bid	BH3 interacting domain death agonist	71836838	12122	NM_007544.2
Blcap	bladder cancer associated protein homolog (human)	71016617	53619	NM_016916.2
Blnk	B-cell linker	74819692	17060	NM_008528.3
Bmp3	bone morphogenetic protein 3	72472749	110075	NM_173404.1
Bmp4	bone morphogenetic protein 4	1333	12159	NM_007554
Bmp4	bone morphogenetic protein 4	1671	12159	NM_007554
Bmp5	bone morphogenetic protein 5	73817428	12160	NM_007555.1
Bmp7	bone morphogenetic protein 7	2065	12162	NM_007557
Bnc2	basonuclin 2	73636164	242509	NM_172870.3
Bnip3	BCL2/adenovirus E1B interacting protein 1, NIP3	75077193	12176	NM_009760.2
Boc	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein	74819594	117606	NM_172506.1
Bok	Bcl-2-related ovarian killer protein	71064032	51800	NM_016778.1
Bpgm	2,3-bisphosphoglycerate mutase	67936202	12183	NM_007563.2
Bpgm	2,3-bisphosphoglycerate mutase	77414641	12183	NM_007563.2
Brd8	bromodomain containing 8	1673	78656	NM_030147
Brp17	paroxysmal nonkinesigenic dyskinesia	73769326	56695	NM_019999.1
Brp44l	brain protein 44-like	2067	55951	NM_018819
Brs3	bombesin-like receptor 3	70560328	12209	NM_009766.2

Brunol4	bruno-like 4, RNA binding protein (Drosophila)	73592527	108013	NM_133195.1
Brunol6	bruno-like 6, RNA binding protein (Drosophila)	71358616	76183	NM_175235.3
Bsdc1	BSD domain containing 1	74988722	100383	NM_133889.2
Bsg	basigin	166	12215	NM_009768
Bsn	bassoon	73992923	12217	NM_007567.1
Btbd11	BTB (POZ) domain containing 11	73769325	74007	XM_125798.4
Btbd14a	BTB (POZ) domain containing 14A	70743871	67991	NM_026495.2
Btbd3	BTB (POZ) domain containing 3	71016618	228662	NM_145534.1
Btd	biotinidase	2069	26363	NM_025295
Btg1	B-cell translocation gene 1, anti-proliferative	73718576	12226	NM_007569.1
Btg2	B-cell translocation gene 2, anti-proliferative	72283802	12227	NM_007570.1
Btg3	B-cell translocation gene 3	72008120	12228	NM_009770.1
Btg3	B-cell translocation gene 3	168	12228	NM_009770
Btrc	beta-transducin repeat containing protein	74047905	12234	NM_009771.1
Bves	blood vessel epicardial substance	74511935	23828	NM_024285.1
Bxdc1	brix domain containing 1	293465	67239	NM_023323.2
Bzrp	translocator protein	2071	12257	NM_009775
Bzw1	basic leucine zipper and W2 domains 1	324215	66882	NM_025824.2
C030002O17Rik		76115725	78533	NM_172432.1
C030003D03Rik	RIKEN cDNA C030003D03 gene	73992712	77220	XM_282904.3
C030014K22Rik	RIKEN cDNA C030014K22 gene	72472750	226610	NM_175461.2
C030019F02Rik	Na <sup>+</sup> /K <sup>+</sup> transporting ATPase interacting 4	1474	58237	NM_021426
C030033F14Rik		2073		
C030034I22Rik	RIKEN cDNA C030034I22 gene	72472751	77533	XM_488832.1
C030038J10Rik	GPRIN family member 3	73520968	243385	NM_183183.1
C030046I01Rik	RIKEN cDNA C030046I01 gene	74881890	109284	NM_177994.2
C030048B12Rik	phosphatidic acid phosphatase type 2 domain containing 1A	74881927	381925	XM_355946.2
C130018E23Rik		75144623		
C130021I20	Riken cDNA C130021I20 gene	74511997	329385	NM_177842.2
C130034I18Rik	RIKEN cDNA C130034I18 gene	72472752	320701	NM_177233.4
C130036G08	transmembrane protein 130	73930834	243339	NM_177735.3
C130038G02Rik	RIKEN cDNA C130038G02 gene	70431434	77521	NM_029920.3
C130052I12Rik	CLPTM1-like	1675	218335	NM_146047
C130060K24Rik	RIKEN cDNA C130060K24 gene	1164	243407	NM_175524
C130076O07Rik	neuron-glia-CAM-related cell adhesion molecule	172	319504	NM_176930
C130090K23Rik	RIKEN cDNA C130090K23 gene	74819236	231293	NM_145560.1
C130096N06Rik		73635978	320220	XM_484001.1
C1qa	complement component 1, q subcomponent, alpha polypeptide	77371775	12259	NM_007572.1
C1qc	complement component 1, q subcomponent, C chain	77340474	12262	NM_007574.1
C1qtnf3	C1q and tumor necrosis factor related protein 3	75041550	81799	NM_030888.2
C1qtnf5	C1q and tumor necrosis factor related protein 5	293664	235312	NM_145613.2
C1r	complement component 1, r subcomponent	70813896	50909	NM_023143.1
C1r	complement component 1, r subcomponent	77874604	50909	NM_023143.1
C230009H10Rik		72472761	320399	NM_177153.2
C230030N03Rik	RIKEN cDNA C230030N03 gene	73992924	241052	NM_172847.1
C230040D10Rik	myosin XVI	73520969	244281	XM_356059.2
C230069K22Rik	coiled-coil domain containing 37	74581372	243538	NM_173775.2
C230071H18Rik	RIKEN cDNA C230071H18 gene	72283803	399569	NM_207265.1
C230079D11Rik	additional sex combs like 3 (Drosophila)	74988269	211961	XM_140204.4

C230081A13Rik	RIKEN cDNA C230081A13 gene	73931624	244895	NM_172924.1
C230095G01Rik	RIKEN cDNA C230095G01 gene	73992925	319776	NM_178768.3
C230098I05Rik	GSG1-like	73636097	269994	XM_194378.4
C330005L02Rik	solute carrier family 25, member 36	67881555	192287	NM_138756.2
C330005M16Rik	RIKEN cDNA C330005M16 gene	74272930	101744	NM_175319.2
C330014O21Rik	transmembrane protein 86B	72472763	68255	XM_486035.1
C330016H24Rik	serologically defined colon cancer antigen 3	2075		NM_026563
C330017I15Rik	pseudouridylate synthase 7 homolog (S. cerevisiae)	356854	78697	NM_178403.2
C4	complement component 4B (Chido blood group)	74047758	12268	NM_009780.1
C530008M17Rik	RIKEN cDNA C530008M17 gene	75080646	320827	
C630002B14Rik	5'-nucleotidase domain containing 3	73992926	103466	NM_175331.2
C630007C17Rik	zinc finger protein 804A	73817426	241514	XM_485015.1
C630035N08Rik	RIKEN cDNA C630035N08 gene	73520970	109349	NM_175427.2
C630041L24Rik	serine peptidase inhibitor, Kazal type 8	72129253	78709	NM_183136.1
C730048E16Rik	ankyrin repeat domain 54	1677	223690	NM_144849
C78409	expressed sequence C78409	74273116	216441	NM_177615.2
C79267	expressed sequence C79267	322962	212632	NM_183148.1
C85492	expressed sequence C85492	74658171	215494	NM_153540.2
C920006C10Rik	RIKEN cDNA C920006C10 gene	75749772	76740	NM_133766.1
C920006C10Rik	RIKEN cDNA C920006C10 gene	71015351	76740	NM_133766.1
Cab39l	calcium binding protein 39-like	77371789	69008	NM_026908.2
Cables2	Cdk5 and Abl enzyme substrate 2	72339555	252966	NM_145851.1
Cabp7	calcium binding protein 7	73930835	192650	NM_138948.2
Cacna1e	calcium channel, voltage-dependent, R type, alpha 1E subunit	74988669	12290	NM_009782.2
Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subunit	71587822	12291	NM_009783.1
Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	72119638	58226	NM_021415.2
Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	72119649	12293	NM_009784.1
Cacna2d2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	72119650	56808	NM_020263.2
Cacna2d3	calcium channel, voltage-dependent, alpha2/delta subunit 3	70560338	12294	NM_009785.1
Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	72119651	12296	NM_023116.1
Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	70560340	12297	NM_007581.1
Cacnb4	calcium channel, voltage-dependent, beta 4 subunit	1679	12298	NM_146123
Cacng3	calcium channel, voltage-dependent, gamma subunit 3	73615560	54376	NM_019430.1
Cacng4	calcium channel, voltage-dependent, gamma subunit 4	72119652	54377	NM_019431.1
Cacng5	calcium channel, voltage-dependent, gamma subunit 5	70560341	140723	NM_080644.2
Cacng7	calcium channel, voltage-dependent, gamma subunit 7	74750054	81904	NM_133189.1
Cacng8	calcium channel, voltage-dependent, gamma subunit 8	72108823	81905	NM_133190.1
Cacybp	calcyclin binding protein	75144703	12301	NM_009786.1
Cadps	Ca<2+>dependent activator protein for secretion	72119581	27062	NM_012061.1
Cadps2	Ca2+-dependent activator protein for secretion 2	73817429	320405	NM_153163.2
Calb1	calbindin-28K	69120566	12307	NM_009788.2
Calb1	calbindin-28K	1166	12307	NM_009788
Calb2	calbindin 2	69120619	12308	NM_007586.1
Calb2	calbindin 2	177	12308	NM_007586
Calca	calcitonin/calcitonin-related polypeptide, alpha	71063828	12310	NM_007587.1
Calcb	calcitonin-related polypeptide, beta	72338699	116903	NM_054084.1
Calcr	calcitonin receptor	75080999	12311	NM_007588.1
Calcr1	calcitonin receptor-like	74988670	54598	NM_018782.1
Calm1	calmodulin 1	179	12313	NM_009790

Calm2	calmodulin 2	182	12314	NM_007589
Calm3	calmodulin 3	184	12315	NM_007590
Calml3	calmodulin-like 3	61003	70405	NM_027416.1
Camk1d	calcium/calmodulin-dependent protein kinase ID	73992927	227541	NM_177343.2
Camk1g	calcium/calmodulin-dependent protein kinase I gamma	70743868	215303	NM_144817.1
Camk2a	calcium/calmodulin-dependent protein kinase II alpha	83160	12322	NM_009792.1
Camk2d	calcium/calmodulin-dependent protein kinase II, delta	71016676	108058	NM_023813.2
Camk2g	calcium/calmodulin-dependent protein kinase II gamma	189	12325	NM_178597
Camk4	calcium/calmodulin-dependent protein kinase IV	75038464	12326	NM_009793.1
Camkk1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	73930840	55984	NM_018883.1
Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	70743899	207565	NM_145358.1
Caml	calcium modulating ligand	77280337	12328	NM_007596.1
Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	323396	12331	NM_007598.2
Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	70436737	67252	NM_026056.2
Capn2	calpain 2	73817430	12334	NM_009794.1
Capns1	calpain, small subunit 1	75934915	12336	NM_009795.1
Capsl	calcyphosine-like	75079776	75568	NM_029341.1
Car10	carbonic anhydrase 10	71587832	72605	XM_126517.5
Car12	carbonic anhydrase 12	72081406	76459	NM_178396.3
Car2	carbonic anhydrase 2	72103831	12349	NM_009801.3
Car4	carbonic anhydrase 4	70928238	12351	NM_007607.1
Car7	carbonic anhydrase 7	74511736	12354	NM_053070.1
Car8	carbonic anhydrase 8	191	12319	NM_007592
Car9	carbonic anhydrase 9	74988271	230099	NM_139305.1
Card15	nucleotide-binding oligomerization domain containing 2	75038483	257632	NM_145857.1
Carhsp1	calcium regulated heat stable protein 1	73512493	52502	NM_025821.2
Cart	CART prepropeptide	72077479	27220	NM_013732.3
Casc1	cancer susceptibility candidate 1	75038484	320662	NM_177222.3
Casp9	caspase 9	1681	12371	NM_015733
Casq1	calsequestrin 1	74819254	12372	NM_009813.1
Casq2	calsequestrin 2	76115726	12373	NM_009814.1
Casr	calcium-sensing receptor	72338697	12374	NM_013803.1
Cast	calpastatin	70928199	12380	NM_009817.1
Catnb	catenin (cadherin associated protein), beta 1	196		NM_007614
Catnbip1	catenin beta interacting protein 1	70805935	67087	NM_023465.2
Cbara1	calcium binding atopy-related autoantigen 1	74658238	216001	NM_144822.1
Cbfa2t3h	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 homolog (human)	75038485	12398	NM_009824.1
Cbfb	core binding factor beta	1168	12400	NM_022309
Cblb	Casitas B-lineage lymphoma b	74988451	208650	XM_358863.2
Cbln2	cerebellin 2 precursor protein	70231306	12405	NM_172633.1
Cbln4	cerebellin 4 precursor protein	72283804	228942	NM_175631.1
Cbr3	carbonyl reductase 3	2077	109857	NM_173047
Cbs	cystathionine beta-synthase	1335	12411	NM_144855
Cbx5	chromobox homolog 5 (Drosophila HP1a)	198	12419	NM_007626
Ccbp2	chemokine binding protein 2	74724637	59289	NM_021609.2
Ccdc3	coiled-coil domain containing 3	75651160	74186	XM_129987.3
Cck	cholecystokinin	200	12424	NM_031161
Cck	cholecystokinin	77869074	12424	NM_031161.1
Cckar	cholecystokinin A receptor	203	12425	NM_009827



Cckbr	cholecystokinin B receptor	70560342	12426	NM_007627.2
Ccnd2	cyclin D2	205	12444	NM_009829
Ccng1	cyclin G1	324210	12450	NM_009831.1
Ccni	cyclin I	74988529	12453	NM_017367.2
Ccnl2	cyclin L2	211	56036	NM_018856
Ccr1	chemokine (C-C motif) receptor 1	73718058	12768	NM_009912.2
Cct2	chaperonin subunit 2 (beta)	356082	12461	NM_007636.1
Cct8	chaperonin subunit 8 (theta)	2079	12469	NM_009840
Cd109	CD109 antigen	73931384	235505	NM_153098.2
Cd164	CD164 antigen	75749771	53599	NM_016898.1
Cd1d1	CD1d1 antigen	219	12479	NM_007639
Cd200	Cd200 antigen	71358579	17470	NM_010818.2
Cd24a	CD24a antigen	73787950	12484	NM_009846.1
Cd24a	CD24a antigen	73787951	12484	NM_009846.1
Cd33	CD33 antigen	75043153	12489	NM_021293.1
Cd34	CD34 antigen	74047898	12490	NM_133654.1
Cd4	CD4 antigen	74819249	12504	NM_013488.1
Cd44	CD44 antigen	224	12505	NM_009851
Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	357100	16423	NM_010581.3
Cd59a	CD59a antigen	73992928	12509	NM_007652.2
Cd6	CD6 antigen	357101	12511	NM_009852.1
Cd63	Cd63 antigen	73992715	12512	NM_007653.1
Cd81	CD 81 antigen	226	12520	NM_133655
Cd8b1	CD8 antigen, beta chain 1	73732149	12526	NM_009858.1
Cd9	CD9 antigen	73520971	12527	NM_007657.3
Cd97	CD97 antigen	2081	26364	NM_011925
Cda	cytidine deaminase	74425539	72269	XM_131801.2
Cdc25b	cell division cycle 25 homolog B (S. pombe)	74274686	12531	NM_023117.1
Cdc27	cell division cycle 27 homolog (S. cerevisiae)	293466	217232	XM_484088.1
Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	70814345	104445	NM_027219.1
Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	75146001	260409	NM_026514.1
Cdca2	cell division cycle associated 2	73520972	108912	NM_175384.3
Cdca7	cell division cycle associated 7	26	66953	NM_025866
Cdgap	Cdc42 GTPase-activating protein	73512366	12549	NM_020260.1
Cdh10	cadherin 10	73592529	320873	XM_283264.3
Cdh10	cadherin 10	230	320873	
Cdh11	cadherin 11	74881285	12552	NM_009866.3
Cdh11	cadherin 11	232	12552	NM_009866
Cdh13	cadherin 13	234	12554	NM_019707
Cdh13	cadherin 13	77869863	12554	NM_019707.1
Cdh15	cadherin 15	77869780	12555	NM_007662.1
Cdh2	cadherin 2	236	12558	NM_007664
Cdh23	cadherin 23 (otocadherin)	72283805	22295	NM_023370.1
Cdh24	cadherin-like 24	70231307	239096	NM_199470.1
Cdh3	cadherin 3	1337	12560	NM_007665
Cdh4	cadherin 4	72008309	12561	NM_009867.1
Cdh4	cadherin 4	2083	12561	NM_009867
Cdh6	cadherin 6	238	12563	NM_007666
Cdh7	cadherin 7, type 2	73520973	241201	NM_172853.1

Cdh8	cadherin 8	72081552	12564	NM_007667.1
Cdh8	cadherin 8	240	12564	NM_007667
Cdh9	cadherin 9	72472764	12565	XM_487374.1
Cdk5	cyclin-dependent kinase 5	244	12568	NM_007668
Cdk5r1	cyclin-dependent kinase 5, regulatory subunit (p35) 1	247	12569	NM_009871
Cdk8	cyclin-dependent kinase 8	75147769	264064	NM_153599.2
Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	2085	12575	NM_007669
Cdkn1b	cyclin-dependent kinase inhibitor 1B	356491	12576	NM_009875.2
Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	1476	12579	NM_007670
Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1683	12580	NM_007671
Cdkn2d	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	1603	12581	NM_009878
Cdo1	cysteine dioxygenase 1, cytosolic	74583197	12583	NM_033037.2
Cdr2	cerebellar degeneration-related 2	73992716	12585	NM_007672.1
Cds1	CDP-diacylglycerol synthase 1	72103808	74596	NM_173370.3
Cds2	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2	250	110911	NM_138651
Cdyl2	chromodomain protein, Y chromosome-like 2	74641321	75796	NM_029441.1
Ceacam14	CEA-related cell adhesion molecule 14	75080228	67084	NM_025957.2
Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	2087	12606	NM_007678
Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	76115722	12609	NM_007679.2
Celsr3	cadherin EGF LAG seven-pass G-type receptor 3	74724639	107934	NM_080437.1
Cenpf	centromere protein F	1631	108000	XM_129658
Centa1	centaurin, alpha 1	74658055	231821	NM_172723.1
Centd1	centaurin, delta 1	74881937	212285	XM_132099.6
Centg3	centaurin, gamma 3	2089	213990	NM_139153
Cer1	cerberus 1 homolog (Xenopus laevis)	2091	12622	NM_009887
Cerk	ceramide kinase	72472765	223753	NM_145475.2
Cgnl1	cingulin-like 1	72008123	68178	NM_026599.3
Chat	choline acetyltransferase	252	12647	NM_009891
Chchd2	coiled-coil-helix-coiled-coil-helix domain containing 2	74272036	14004	NM_024166.4
Chchd3	coiled-coil-helix-coiled-coil-helix domain containing 3	67870084	66075	NM_025336.1
Chd2	chromodomain helicase DNA binding protein 2	255	69959	XM_145698
Chd5	chromodomain helicase DNA binding protein 5	72283806	269610	XM_196334.4
Chd6	chromodomain helicase DNA binding protein 6	77340492	71389	TC1498207.1
Chd7	chromodomain helicase DNA binding protein 7	71836884	320790	XM_149413.4
Chga	chromogranin A	2093	12652	NM_007693
Chgb	chromogranin B	70743886	12653	NM_007694.1
Chl1	cell adhesion molecule with homology to L1CAM	74272476	12661	NM_007697.1
Chml	choroideremia-like	74047442	12663	NM_021350.1
Chn1	chimerin (chimaerin) 1	73718053	108699	NM_029716.1
Chn2	chimerin (chimaerin) 2	74881162	69993	NM_023543.1
Chn2	chimerin (chimaerin) 2	77280428	69993	NM_023543.1
Chrd	chordin	257	12667	NM_009893
Chrm1	cholinergic receptor, muscarinic 1, CNS	73907497	12669	NM_007698.2
Chrm2	cholinergic receptor, muscarinic 2, cardiac	70560343	243764	NM_203491.1
Chrm3	cholinergic receptor, muscarinic 3, cardiac	2095	12671	NM_033269
Chrm4	cholinergic receptor, muscarinic 4	261	12672	NM_007699
Chrm4	cholinergic receptor, muscarinic 4	259	12672	NM_007699
Chrm5	cholinergic receptor, muscarinic 5	75826557	213788	NM_205783.1
Chrna1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	75551465	11435	NM_007389.2

Chrna2	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	75551460	110902	NM_144803.1
Chrna3	cholinergic receptor, nicotinic, alpha polypeptide 3	72119655	110834	NM_145129.1
Chrna4	cholinergic receptor, nicotinic, alpha polypeptide 4	1173	11438	NM_015730
Chrna5	cholinergic receptor, nicotinic, alpha polypeptide 5	75826567	110835	NM_176844.3
Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6	75651213	11440	NM_021369.2
Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6	75551461	11440	NM_021369.2
Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7	74511738	11441	NM_007390.2
Chrna9	cholinergic receptor, nicotinic, alpha polypeptide 9	75826568	231252	XM_132045.3
Chrnbl	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	75888752	11443	NM_009601.3
Chrnbl	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	2097	11444	NM_009602
Chrnbl	cholinergic receptor, nicotinic, beta polypeptide 3	70436747	108043	NM_027454.1
Chrnbl	cholinergic receptor, nicotinic, beta polypeptide 4	264	108015	NM_148944
Chrnd	cholinergic receptor, nicotinic, delta polypeptide	74988680	11447	NM_021600.1
Chrne	cholinergic receptor, nicotinic, epsilon polypeptide	75888738	11448	NM_009603.1
Chrng	cholinergic receptor, nicotinic, gamma polypeptide	75551466	11449	NM_009604.2
Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	71836872	76969	NM_023850.1
Chst10	carbohydrate sulfotransferase 10	74657931	98388	NM_145142.1
Chst11	carbohydrate sulfotransferase 11	73931625	58250	NM_021439.1
Chst12	carbohydrate sulfotransferase 12	74881144	59031	NM_021528.2
Chst2	carbohydrate sulfotransferase 2	266	54371	NM_018763
Chst8	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 8	72080187	68947	NM_175140.3
Chuk	conserved helix-loop-helix ubiquitous kinase	1685	12675	NM_007700
Chx10	visual system homeobox 2	1687	12677	NM_007701
Cib2	calcium and integrin binding family member 2	71836803	56506	NM_019686.3
Cidea	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	73992929	12683	NM_007702.1
Cirh1a	cirrhosis, autosomal recessive 1A (human)	77925143	21771	NM_011574.1
Cish	cytokine inducible SH2-containing protein	70634310	12700	NM_009895.2
Cit	citron	75079801	12704	NM_007708.1
Cited1	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1	74641326	12705	NM_007709.3
Ckap2	cytoskeleton associated protein 2	74363353	80986	NM_001004140.1
Ckb	creatine kinase, brain	70927826	12709	NM_021273.2
Cklfsf3	CKLF-like MARVEL transmembrane domain containing 3	2099		NM_024217
Cklfsf4	CKLF-like MARVEL transmembrane domain containing 4	2101		NM_153582
Ckm	creatine kinase, muscle	76115727	12715	NM_007710.1
Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	270	12716	NM_009897
Cks2	CDC28 protein kinase regulatory subunit 2	74512038	66197	NM_025415.1
Clca1	chloride channel calcium activated 1	2105	12722	NM_009899
Clca2	chloride channel calcium activated 2	70301278	80797	NM_030601.2
Clcn2	chloride channel 2	72119656	12724	NM_009900.1
Clcn5	chloride channel 5	75749741	12728	NM_016691.2
Cldn1	claudin 1	70612723	12737	NM_016674.2
Cldn11	claudin 11	77280580	18417	NM_008770.1
Cldn12	claudin 12	2107	64945	NM_022890
Clgn	calmegin	74425567	12745	NM_009904.1
Clic1	chloride intracellular channel 1	67809267	114584	NM_033444.1
Clic4	chloride intracellular channel 4 (mitochondrial)	73769125	29876	NM_013885.1
Clic5	chloride intracellular channel 5	73636094	224796	NM_172621.1
Clic5	chloride intracellular channel 5	77874610	224796	NM_172621.1
Clic6	chloride intracellular channel 6	1984	209195	NM_172469

Clk2	CDC-like kinase 2	356286	12748	NM_007712.1
Clmn	calmin	73931626	94040	NM_053155.1
Clns1a	chloride channel, nucleotide-sensitive, 1A	67881553	12729	NM_023671.1
Clock	circadian locomoter output cycles kaput	273	12753	NM_007715
Clptm1	cleft lip and palate associated transmembrane protein 1	544901	56457	NM_019649.1
Clstn1	calsyntenin 1	73769319	65945	NM_023051.1
Clstn2	calsyntenin 2	73636091	64085	NM_022319.2
Clta	clathrin, light polypeptide (Lca)	74819690	12757	NM_016760.1
Clu	clusterin	275	12759	NM_013492
Cmklr1	chemokine-like receptor 1	72340129	14747	NM_008153.1
Cnih	cornichon homolog (Drosophila)	278	12793	NM_009919
Cnil	cornichon homolog 2 (Drosophila)	2109		NM_009920
Cnksr3	Cnksr family member 3	74273121	215748	NM_172546.1
Cnnm1	cyclin M1	73992930	83674	NM_031396.1
Cnnm2	cyclin M2	74581378	94219	NM_033569.1
Cnot7	CCR4-NOT transcription complex, subunit 7	321203	18983	NM_011135.2
Cnp1	2',3'-cyclic nucleotide 3' phosphodiesterase	1175	12799	NM_009923
Cnp1	2',3'-cyclic nucleotide 3' phosphodiesterase	77371841	12799	NM_009923.1
Cnr1	cannabinoid receptor 1 (brain)	283	12802	NM_007726
Cnr2	cannabinoid receptor 2 (macrophage)	2111	12802	NM_009924
Cntfr	ciliary neurotrophic factor receptor	75651138	12804	NM_016673.1
Cntn1	contactin 1	414	12805	NM_007727
Cntn3	contactin 3	73992717	18488	NM_008779.1
Cntn4	contactin 4	73992718	269784	NM_173004.1
Cntn6	contactin 6	74882147	53870	NM_017383.3
Cntnap1	contactin associated protein-like 1	73992931	53321	NM_016782.1
Cntnap2	contactin associated protein-like 2	544712	66797	NM_001004357.0
Cntnap4	contactin associated protein-like 4	70928361	170571	NM_130457.2
Coch	coagulation factor C homolog (Limulus polyphemus)	71717614	12810	NM_007728.2
Col10a1	procollagen, type X, alpha 1	74581398	12813	NM_009925.1
Col11a1	procollagen, type XI, alpha 1	71064195	12814	NM_007729.1
Col12a1	procollagen, type XII, alpha 1	73817431	12816	NM_007730.1
Col14a1	procollagen, type XIV, alpha 1	74658056	12818	NM_181277.1
Col15a1	procollagen, type XV	74511791	12819	NM_009928.2
Col16a1	procollagen, type XVI, alpha 1	74273122	107581	NM_028266.3
Col18a1	procollagen, type XVIII, alpha 1	287	12822	NM_009929
Col19a1	procollagen, type XIX, alpha 1	74658066	12823	NM_007733.1
Col23a1	procollagen, type XXIII, alpha 1	73636092	237759	NM_153393.1
Col24a1	procollagen, type XXIV, alpha 1	73636093	71355	XM_355436.2
Col25a1	procollagen, type XXV, alpha 1	71924301	77018	NM_029838.3
Col27a1	procollagen, type XXVII, alpha 1	74272916	373864	NM_025685.2
Col4a2	procollagen, type IV, alpha 2	73592540	12827	NM_009932.2
Col4a5	procollagen, type IV, alpha 5	73992932	12830	NM_007736.1
Col4a6	procollagen, type IV, alpha 6	72103841	94216	NM_053185.1
Col5a1	procollagen, type V, alpha 1	75147768	12831	NM_015734.1
Col5a2	procollagen, type V, alpha 2	71016666	12832	NM_007737.1
Col5a3	procollagen, type V, alpha 3	74272917	53867	NM_016919.1
Col6a1	procollagen, type VI, alpha 1	290	12833	NM_009933
Col6a1	procollagen, type VI, alpha 1	77869097	12833	NM_009933.1

Col6a2	procollagen, type VI, alpha 2	1177	12834	NM_146007
Col6a3	procollagen, type VI, alpha 3	75081393	12835	XM_484897.2
Col9a1	procollagen, type IX, alpha 1	71064061	12839	NM_007740.2
Col9a2	procollagen, type IX, alpha 2	74750022	12840	NM_007741.1
Col9a3	procollagen, type IX, alpha 3	70928304	12841	NM_009936.1
Copa	coatamer protein complex subunit alpha	1689	12847	NM_009938
Copb2	coatamer protein complex, subunit beta 2 (beta prime)	1341	50797	NM_015827
Copg	coatamer protein complex, subunit gamma	67779873	54161	NM_017477.1
Copg2	coatamer protein complex, subunit gamma 2	74819259	54160	NM_017478.2
Cops4	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	74882166	26891	NM_012001.1
Cops7b	COP9 (constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana)	356493	26895	NM_172974.1
Copz2	coatamer protein complex, subunit zeta 2	275874	56358	NM_019877.1
Coro1c	coronin, actin binding protein 1C	75651191	23790	NM_011779.2
Coro2b	coronin, actin binding protein, 2B	72077454	235431	NM_175484.1
Coro6	coronin, actin binding protein 6	77280432	216961	NM_139128.1
Cort	cortistatin	72472766	12854	NM_007745.2
Cotl1	coactosin-like 1 (Dictyostelium)	72472769	72042	NM_028071.1
Cova1	ecto-NOX disulfide-thiol exchanger 2	70928339	209224	NM_145951.2
Cox4i1	cytochrome c oxidase subunit IV isoform 1	73992933	12857	NM_009941.1
Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	71836876	12862	NM_009943.1
Cox6c	cytochrome c oxidase, subunit VIc	74641307	12864	NM_053071.1
Cox7b	cytochrome c oxidase subunit VIIb	67870085	66142	NM_025379.1
Cpe	carboxypeptidase E	1691	12876	NM_013494
Cpeb1	cytoplasmic polyadenylation element binding protein 1	72472770	12877	NM_007755.1
Cplx1	complexin 1	67752308	12889	NM_007756.2
Cpne2	copine II	70743844	234577	NM_153507.2
Cpne3	copine III	74988745	70568	NM_027769.1
Cpne5	copine V	544709	240058	NM_153166.1
Cpne6	copine VI	73769322	12891	NM_009947.2
Cpne7	copine VII	73817432	102278	NM_170684.1
Cpne8	copine VIII	73520974	66871	NM_025815.1
Cpsf5	nudix (nucleoside diphosphate linked moiety X)-type motif 21	2115		NM_026623
Cpt1a	carnitine palmitoyltransferase 1a, liver	1478	12894	NM_013495
Cpt1c	carnitine palmitoyltransferase 1c	2117	78070	NM_153679
Crabp1	cellular retinoic acid binding protein I	1179	12903	NM_013496
Crat	carnitine acetyltransferase	2119	12908	NM_007760
Creb3l1	cAMP responsive element binding protein 3-like 1	1693	26427	NM_011957
Creg1	cellular repressor of E1A-stimulated genes 1	73931627	433375	NM_011804.2
Creg2	cellular repressor of E1A-stimulated genes 2	74882195	263764	NM_170597.3
Crh	corticotropin releasing hormone	292	12918	NM_205769
Crhr1	corticotropin releasing hormone receptor 1	297	12921	NM_007762
Crhr2	corticotropin releasing hormone receptor 2	2121	12922	NM_009953
Cri1	EP300 interacting inhibitor of differentiation 1	74583118	58521	NM_025613.1
Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	72283807	50766	XM_128751.5
Crip2	cysteine rich protein 2	70612727	68337	NM_024223.1
Crispld1	cysteine-rich secretory protein LCCL domain containing 1	72077456	83691	NM_031402.1
Crllf1	cytokine receptor-like factor 1	72283808	12931	NM_018827.1
Crllf3	cytokine receptor-like factor 3	2123	54394	NM_018776
Crry	complement receptor related protein	2125	12946	NM_013499

Crsp3	mediator complex subunit 23	61004	70208	XM_358301.2
Crsp7	mediator complex subunit 26	73992934	70625	NM_027485.1
Crtac1	cartilage acidic protein 1	75749739	72832	NM_145123.2
Cry2	cryptochrome 2 (photolyase-like)	302	12953	NM_009963
Cryaa	crystallin, alpha A	2127	12954	NM_013501
Crym	crystallin, mu	73592526	12971	NM_016669.1
Cryz1	crystallin, zeta (quinone reductase)-like 1	304	66609	NM_133679
Cs	citrate synthase	74658130	12974	NM_026444.2
Csdc2	cold shock domain containing C2, RNA binding	77887884	105859	NM_145473.1
Csen	Kv channel interacting protein 3, calsenilin	71587887	56461	NM_019789.2
Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	73992937	12984	NM_007781.1
Csk	c-src tyrosine kinase	75651192	12988	NM_007783.2
Csnk1a1	casein kinase 1, alpha 1	74658110	93687	NM_146087.1
Cspg2	versican	73520975	13003	XM_488510.1
Cspg5	chondroitin sulfate proteoglycan 5	73931385	29873	NM_013884.2
Csrp1	cysteine and glycine-rich protein 1	2129	13007	NM_007791
Csrp2bp	cysteine and glycine-rich protein 2 binding protein	276275	228714	NM_181417.2
Csrp3	cysteine and glycine-rich protein 3	77332671	13009	NM_013808.3
Cst3	cystatin C	69120555	13010	NM_009976.2
Cst6	cystatin E/M	75041560	73720	NM_028623.2
Cstb	cystatin B	1343	13014	NM_007793
Cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	2131	108062	NM_133196
Ctag3	cancer antigen 1	72472771	71213	XM_356655.2
Ctbp2	C-terminal binding protein 2	70615583	13017	NM_009980.2
Ctf1	cardiotrophin 1	1695	13019	NM_007795
Ctgf	connective tissue growth factor	1183	14219	NM_010217
Cth	cystathionase (cystathionine gamma-lyase)	75042264	107869	NM_145953.2
Cthrc1	collagen triple helix repeat containing 1	72472772	68588	XM_128002.4
Ctla4	cytotoxic T-lymphocyte-associated protein 4	75079745	12477	NM_009843.2
Ctnna2	catenin (cadherin associated protein), alpha 2	74363355	12386	NM_009819.1
Ctnnd1	catenin (cadherin associated protein), delta 1	74641320	12388	NM_007615.1
Ctps	cytidine 5'-triphosphate synthase	1185	51797	NM_016748
Ctsb	cathepsin B	67779877	13030	NM_007798.1
Ctsl	cathepsin L	1187	13039	NM_009984
Ctss	cathepsin S	77371797	13040	NM_021281.1
Ctsw	cathepsin W	75041420	13041	NM_009985.2
Ctsz	cathepsin Z	71015377	64138	NM_022325.3
Cttn	cortactin	70616018	13043	NM_007803.1
Ctxn1	cortexin 1	74586669	330695	NM_183315.1
Cubn	cubilin (intrinsic factor-cobalamin receptor)	75041430	65969	XM_130038.3
Cuedc2	CUE domain containing 2	67755428	67116	NM_024192.1
Cul4a	cullin 4A	75749399	99375	NM_146207.1
Cutl1	cut-like 1 (Drosophila)	2133	13047	NM_009986
Cutl2	cut-like 2 (Drosophila)	72128748	13048	NM_007804.2
Cx3cl1	chemokine (C-X3-C motif) ligand 1	2135	20312	NM_009142
Cx3cr1	chemokine (C-X3-C) receptor 1	1605	13051	NM_009987
Cxcl12	chemokine (C-X-C motif) ligand 12	308	20315	NM_013655
Cxcl13	chemokine (C-X-C motif) ligand 13	74819234	55985	NM_018866.1
Cxcl14	chemokine (C-X-C motif) ligand 14	74272041	57266	NM_019568.1

Cyb5	cytochrome b-5	75043146	109672	NM_025797.1
Cyb561	cytochrome b-561	71020402	13056	NM_007805.2
Cyc1	cytochrome c-1	357103	66445	NM_025567.1
Cyfp1	cytoplasmic FMR1 interacting protein 1	74819653	20430	NM_011370.1
Cygb	cytoglobin	72103830	114886	NM_030206.1
Cyhr1	cysteine and histidine rich 1	293033	54151	NM_019396.1
Cyhr1	cysteine and histidine rich 1	77414565	54151	NM_019396.1
Cyld	cylindromatosis (turban tumor syndrome)	73992938	74256	NM_173369.1
Cyln2	CAP-GLY domain containing linker protein 2	2137	269713	NM_009990
Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	72081548	232174	NM_175475.2
Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	310	232174	NM_175475
Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	70634300	104086	NM_024264.3
Cyp2j6	cytochrome P450, family 2, subfamily j, polypeptide 6	77278979	13110	NM_010008.2
Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	71836847	56050	NM_018887.2
Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	77874608	56050	NM_018887.2
Cyp46a1	cytochrome P450, family 46, subfamily a, polypeptide 1	70613977	13116	NM_010010.1
Cyp4f15	cytochrome P450, family 4, subfamily f, polypeptide 15	1189	106648	NM_134127
Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	74882196	102294	NM_133969.1
Cyp51	cytochrome P450, family 51	75934914	13121	NM_020010.1
Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	70927813	13123	NM_007825.1
Cyr61	cysteine rich protein 61	1191	16007	NM_010516
Cyslrl	cysteinyl leukotriene receptor 1	75651227	58861	NM_021476.2
D030063F01Rik		73931628	320269	NM_177122.2
D0H4S114	DNA segment, human D4S114	72472773	27528	NM_053078.3
D0HXS9928E	DNA segment, human DXS9928E	74882206	108160	NM_138607.1
D10Bwg0791e	TSPY-like 4	67936212	72480	NM_030203.1
D10Bwg1379e	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	75988646	215821	XM_125524.6
D10Ert641e	DNA segment, Chr 10, ERATO Doi 641, expressed	293463	52717	NM_025514.1
D11Bwg0434e	DNA segment, Chr 11, Brigham & Women's Genetics 0434 expressed	75934529	52898	NM_173742.1
D11Ert333e	solute carrier family 25, member 39	74988740	68066	NM_026542.1
D11Ert759e		74881365	268513	NM_172949.1
D11Wsu47e	DNA segment, Chr 11, Wayne State University 47, expressed	74819575	276852	NM_177777.3
D12Ert553e	DNA segment, Chr 12, ERATO Doi 553, expressed	74425565	76820	NM_029758.3
D12Ert771e	SET domain containing 3	74047910	52690	NM_028262.1
D130067103Rik	thrombospondin, type I, domain containing 7B	71358617	210417	NM_172485.2
D130072O21Rik		72472775	102143	NM_175322.2
D130073L02Rik	coiled-coil domain containing 109A	72472776	215999	XM_125687.3
D13Bwg1146e	regulator of G-protein signalling 7 binding protein	73931629	52882	NM_029879.1
D15Bwg0669e	metallophosphoesterase domain containing 1	70231303	223726	NM_172610.1
D15Bwg0759e	FAD-dependent oxidoreductase domain containing 2	74363342	239554	XM_354922.2
D15Ert785e	non-SMC condensin II complex, subunit H2	355887	52683	NM_025795.2
D15Wsu169e	DNA segment, Chr 15, Wayne State University 169, expressed	73992939	223666	NM_198420.1
D16Ert472e	DNA segment, Chr 16, ERATO Doi 472, expressed	318	67102	NM_025967
D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed	74047888	27883	NM_138583.1
D18Ert653e	DNA segment, Chr 18, ERATO Doi 653, expressed	73817443	52662	NM_172631.2
D19Ert703e	SAPS domain family, member 3	356861	52036	NM_029456.1
D1Bwg0491e	transmembrane protein 131	74882216	56030	NM_018872.1
D230050A05	predicted gene, EG208426	74272918	208426	NM_177585.2
D2Bwg0891e	dysbindin (dystrobrevin binding protein 1) domain containing 2	45668	52840	NM_026797.1

D2Bwg1356e	thioredoxin domain containing 13	74882217	52837	XM_130523.4
D330001F17Rik	RIKEN cDNA D330001F17 gene	73992940	223658	XM_283282.3
D330017J20Rik	RIKEN cDNA D330017J20 gene	72283809	320609	NM_177204.2
D330027P03Rik		75144624		
D330050I23Rik	RIKEN cDNA D330050I23 gene	75081395	399603	NM_207269.1
D3Bwg0562e	DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed	73992941	229791	NM_177664.3
D430025H09Rik	leucine rich repeat containing 49	70634108	102747	NM_145616.2
D430038H04Rik	FAT tumor suppressor homolog 3 (Drosophila)	73992719	270120	XM_194446.3
D430041D05Rik	RIKEN cDNA D430041D05 gene	72472777	241589	XM_141380.4
D4Bwg1540e	UBX domain containing 5	322		NM_026257
D4st1	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	74657927	72136	NM_028117.2
D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	74819463	27981	NM_023665.2
D530033C11Rik	RIKEN cDNA D530033C11 gene	71924008	78581	NM_030132.2
D5Bwg0834e	coiled-coil domain containing 92	74658111	215707	NM_144819.1
D5Bwg0860e	RUN and FYVE domain containing 3	73817983	52822	NM_027530.2
D630023B12Rik	RIKEN cDNA D630023B12 gene	74882227	329679	XM_355440.1
D6Wsu176e	DNA segment, Chr 6, Wayne State University 176, expressed	75259443	27999	NM_138587.3
D7Ert156e	nodal modulator 1	1697		NM_153057
D830007F02Rik	RIKEN cDNA D830007F02 gene	73992942	213435	NM_175441.2
D830014K04Rik		75144655		
D830029A09Rik		72472778	414100	XM_484972.1
D830030K20Rik	RIKEN cDNA D830030K20 gene	73930807	320333	NM_177135.2
D8Ert325e	transcription factor 25 (basic helix-loop-helix)	293034	66855	NM_025804.1
D8Ert82e	DNA segment, Chr 8, ERATO Doi 82, expressed	73931630	244418	NM_172911.1
D8Wsu49e	integrin alpha FG-GAP repeat containing 1	2139	71927	NM_028007
D930015E06Rik	RIKEN cDNA D930015E06 gene	1565	229473	NM_172681
D930040M24Rik	I(3)mbt-like 4 (Drosophila)	72472779	320858	NM_177278.2
D9Ert280e	DNA segment, Chr 9, ERATO Doi 280, expressed	72472780	272636	NM_177775.2
Daam2	dishevelled associated activator of morphogenesis 2	74511880	76441	XM_283449.3
Dab1	disabled homolog 1 (Drosophila)	71924090	13131	NM_010014.1
Dach1	dachshund 1 (Drosophila)	74047769	13134	NM_007826.1
Dach2	dachshund 2 (Drosophila)	74819331	93837	NM_033605.1
Dact2	dapper homolog 2, antagonist of beta-catenin (xenopus)	71064219	240025	NM_172826.2
Dad1	defender against cell death 1	74819345	13135	NM_010015.1
Daf2	decay accelerating factor 2	72472783	13137	NM_007827.1
Dag1	dystroglycan 1	355892	13138	NM_010017.1
Dap	death-associated protein	73592541	223453	NM_146057.1
Dapk1	death associated protein kinase 1	72472784	69635	NM_029653.1
Dbh	dopamine beta hydroxylase	326	13166	NM_138942
Dbi	diazepam binding inhibitor	71836880	13167	NM_007830.2
Dbn1	drebrin 1	70928198	56320	NM_019813.2
Dbnl	drebrin-like	74819497	13169	NM_013810.1
Dbp	D site albumin promoter binding protein	1193	13170	NM_016974
Dbr1	debranching enzyme homolog 1 (S. cerevisiae)	2141	83703	NM_031403
Dcamk13	doublecortin-like kinase 3	72079921	245038	NM_172928.1
Dcbl2	discoidin, CUB and LCCL domain containing 2	73992944	73379	NM_028523.2
Dcc	deleted in colorectal carcinoma	72472785	13176	NM_007831.1
Dchs1	dachsous 1 (Drosophila)	72472786	233651	XM_133687.2
Dcn	decorin	329	13179	NM_007833



Dctn6	dynactin 6	323597	22428	NM_011722.1
Ddc	dopa decarboxylase	334	13195	NM_016672
Ddc8	differential display clone 8	73615805	58251	NM_021440.1
Ddef1	development and differentiation enhancing	73512377	13196	NM_010026.1
Ddit4l	DNA-damage-inducible transcript 4-like	71836878	73284	NM_030143.2
Ddr1	discoidin domain receptor family, member 1	72472787	12305	NM_007584.1
Ddr2	discoidin domain receptor family, member 2	74882459	18214	NM_022563.1
Ddt	D-dopachrome tautomerase	75081209	13202	NM_010027.1
Ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	227168	234733	NM_172284.1
Ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	77414162	234733	NM_172284.1
Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	337	13205	NM_010028
Ddx48	eukaryotic translation initiation factor 4A, isoform 3	2143	192170	NM_138669
Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	340	13207	NM_007840
Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	74425550	67460	NM_026172.3
Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	71924363	26378	NM_011933.1
Dedd	death effector domain-containing	70615596	21945	NM_011615.2
Defb1	defensin beta 1	73718051	13214	NM_007843.2
Depdc6	DEP domain containing 6	75749773	97998	NM_145470.1
Depdc6	DEP domain containing 6	76135830	97998	NM_145470.1
Dexi	dexamethasone-induced transcript	73930841	58239	NM_021428.3
Dffa	DNA fragmentation factor, alpha subunit	74819257	13347	NM_010044.1
Dfy	Duffy blood group, chemokine receptor	74581383	13349	NM_010045.1
Dgat2	diacylglycerol O-acyltransferase 2	72077467	67800	NM_026384.2
Dgcr6	DiGeorge syndrome critical region gene 6	73592535	13353	NM_010047.1
Dgkb	diacylglycerol kinase, beta	73787952	217480	NM_178681.2
Dgkb	diacylglycerol kinase, beta	73787953	217480	NM_178681.2
Dgkg	diacylglycerol kinase, gamma	343	110197	NM_138650
Dgkh	diacylglycerol kinase, eta	73992945	380921	XM_484397.1
Dgki	diacylglycerol kinase, iota	74658043	320127	XM_355752.2
Dhcr24	24-dehydrocholesterol reductase	71016721	74754	NM_053272.1
Dhdds	dehydrodolichyl diphosphate synthase	70612728	67422	NM_026144.2
Dhrs3	dehydrogenase/reductase (SDR family) member 3	2145	20148	NM_011303
Dhrs6	3-hydroxybutyrate dehydrogenase, type 2	70806049	69772	NM_027208.1
Dhrs7	dehydrogenase/reductase (SDR family) member 7	75081208	66375	NM_025522.1
Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	73592533	67487	NM_026191.1
Dicer1	Dicer1, Dcr-1 homolog (Drosophila)	74988272	192119	NM_148948.1
Dio3	deiodinase, iodothyronine type III	71717188	107585	NM_172119.1
Dip2		2147		XM_147419
Dip3b	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	72080165	216190	NM_145220.1
Diras1	DIRAS family, GTP-binding RAS-like 1	72103819	208666	NM_145217.2
Dirc2	disrupted in renal carcinoma 2 (human)	72339397	224132	NM_153550.2
Disp2	dispatched homolog 2 (Drosophila)	74511801	214240	NM_170593.1
Dkk1	dickkopf homolog 1 (Xenopus laevis)	2149	13380	NM_010051
Dkk3	dickkopf homolog 3 (Xenopus laevis)	69120613	50781	NM_015814.2
Dkk3	dickkopf homolog 3 (Xenopus laevis)	346	50781	NM_015814
Dkk4	dickkopf homolog 4 (Xenopus laevis)	1480	234130	NM_145592
Dkl1	dickkopf-like 1	70634395	50722	NM_015789.2
Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	70743896	235339	NM_145614.2
Dlgap1	discs, large (Drosophila) homolog-associated protein 1	71924386	224997	NM_027712.2

Dlgap2	discs, large (Drosophila) homolog-associated protein 2	73992720	244310	NM_172910.1
Dlgh2	discs, large homolog 2 (Drosophila)	73817444	23859	NM_011807.1
DLK1	delta-like 1 homolog (Drosophila)	71587885	13386	NM_010052.1
Dist	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	321200	78920	NM_030225.3
Dlx1	distal-less homeobox 1	72008490	13390	NM_010053.1
Dlx1	distal-less homeobox 1	348	13390	NM_010053
Dlx2	distal-less homeobox 2	1482	13392	NM_010054
Dlx3	distal-less homeobox 3	350	13393	NM_010055
Dlx5	distal-less homeobox 5	1450	13395	NM_010056
Dmp1	dentin matrix protein 1	74511936	13406	NM_016779.1
Dmrt3	doublesex and mab-3 related transcription factor 3	74819342	240590	NM_177360.2
Dmwd	dystrophia myotonica-containing WD repeat motif	2151	13401	NM_010058
Dnahc11	dynein, axonemal, heavy chain 11	73520976	13411	NM_010060.1
Dnahc12	dynein, axonemal, heavy chain 12	74988273	110083	XM_486604.1
Dnahc9	dynein, axonemal, heavy chain 9	72472774	237806	XM_110968.4
Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	70744391	58233	NM_021422.2
Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	71836748	81489	NM_018808.1
Dnajb12	DnaJ (Hsp40) homolog, subfamily B, member 12	2153	56709	NM_019965
Dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12	73718054	30045	NM_013888.1
Dnajc6	DnaJ (Hsp40) homolog, subfamily C, member 6	71358627	72685	NM_198412.1
Dnalc4	dynein, axonemal, light chain 4	74047778	54152	NM_017470.1
Dncl2a	dynein light chain roadblock-type 1	323592	67068	NM_025947.1
Dner	delta/notch-like EGF-related receptor	1699	227325	NM_152915
Dnm3	dynamamin 3	74641219	103967	
Dnttip1	deoxynucleotidyltransferase, terminal, interacting protein 1	73718056	76233	NM_133763.1
Doc2a	double C2, alpha	76135829	13446	NM_010069.1
Doc2b	double C2, beta	72283810	13447	NM_007873.2
Doc2g	double C2, gamma	74881341	60425	NM_021791.2
Dock10	dedicator of cytokinesis 10	74047443	210293	XM_129913.5
Dock6	dedicator of cytokinesis 6	75041548	67539	XM_486200.1
Dok1	docking protein 1	75042248	13448	NM_010070.3
Dok2	docking protein 2	2155	13449	NM_010071
Dok4	docking protein 4	1486	114255	NM_053246
Donson	downstream neighbor of SON	2157	60364	NM_021720
Dos	downstream of Stk11	74882515	216164	XM_125771.6
Dp1	receptor accessory protein 5	2159		NM_007874
Dpf3	D4, zinc and double PHD fingers, family 3	72129252	70127	NM_058212.1
Dph2l2	DPH2 homolog (S. cerevisiae)	2161		NM_026344
Dpp10	dipeptidylpeptidase 10	72104183	269109	NM_199021.2
Dpp6	dipeptidylpeptidase 6	75077203	13483	NM_010075.1
Dpy19l1	dpy-19-like 1 (C. elegans)	75042226	244745	NM_172920.1
Dpy19l3	dpy-19-like 3 (C. elegans)	71836886	233115	NM_178704.2
Dpysl3	dihydropyrimidinase-like 3	654928	22240	NM_009468.1
Dpysl4	dihydropyrimidinase-like 4	1345	26757	NM_011993
Dpysl5	dihydropyrimidinase-like 5	73635770	65254	NM_023047.2
Drd1a	dopamine receptor D1A	352	13488	NM_010076
Drd2	dopamine receptor 2	357	13489	NM_010077
Drd3	dopamine receptor 3	75038431	13490	NM_007877.1
Drd4	dopamine receptor 4	2163	13491	NM_007878

Dscr1	regulator of calcineurin 1	362	54720	NM_019466
Dscr11	regulator of calcineurin 2	71064278	53901	NM_030598.2
Dscr5	phosphatidylinositol glycan anchor biosynthesis, class P	2165		NM_019543
Dscr6	ripply3 homolog (zebrafish)	367	170765	NM_133229
Dsp	desmoplakin	76097696	109620	XM_484245.1
Dstn	destrin	74658076	56431	NM_019771.1
Dtna	dystrobrevin alpha	67752311	13527	NM_010087.2
Dtna	dystrobrevin alpha	77413704	13527	NM_010087.2
Dtnbp1	dystrobrevin binding protein 1	75651202	94245	NM_025772.3
Dtx1	deltex 1 homolog (Drosophila)	2167	14357	NM_008052
Dusp1	dual specificity phosphatase 1	324212	19252	NM_013642.1
Dusp10	dual specificity phosphatase 10	73771239	63953	NM_022019.2
Dusp14	dual specificity phosphatase 14	70927831	56405	NM_019819.2
Dusp18	dual specificity phosphatase 18	70634129	75219	NM_173745.4
Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	73512497	72349	NM_028207.1
Dusp4	dual specificity phosphatase 4	72472788	319520	NM_176933.3
Dusp6	dual specificity phosphatase 6	75650864	67603	NM_026268.1
Dvl2	dishevelled 2, dsh homolog (Drosophila)	72103853	13543	NM_007888.1
Dync1li1	dynein cytoplasmic 1 light intermediate chain 1	75774684	235661	NM_146229.1
Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	2169	13548	NM_007890
Dyrk1b	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b	71717583	13549	NM_010092.1
E030007A22	-	74988748	328245	XM_488680.1
E030012M19Rik	layilin	73520977	244864	XM_146887.3
E030013G06Rik	von Willebrand factor A domain containing 3A	72472789	233813	NM_177697.2
E030025D05Rik	coiled-coil domain containing 85A	75081006	216613	NM_181577.2
E130012A19Rik	RIKEN cDNA E130012A19 gene	74363349	103551	NM_175332.2
E130013N09Rik		73992946	99358	XM_488964.1
E130016E03Rik	RIKEN cDNA E130016E03 gene	1488	320890	XM_485355
E130113E03Rik	RIKEN cDNA E130113E03 gene	72472790	319433	XM_127791.4
E130304D01	solute carrier family 10 (sodium/bile acid cotransporter family), member 4	71670742	231290	NM_173403.1
E130307M08Rik	MPN domain containing	75146005	68047	NM_026530.2
E2f1	E2F transcription factor 1	2171	13555	NM_007891
E2f2	E2F transcription factor 2	371	242705	NM_177733
E2f3	E2F transcription factor 3	1490	13557	XM_127250
E2f4	E2F transcription factor 4	67855419	104394	NM_148952.1
E2f4	E2F transcription factor 4	1195	104394	NM_148952
E2f6	E2F transcription factor 6	2173	50496	NM_033270
E330009J07Rik	RIKEN cDNA E330009J07 gene	74658077	243780	NM_175528.2
E330014M11Rik		77280559		
E430002G05Rik	RIKEN cDNA E430002G05 gene	70744322	210622	NM_173749.3
E430012K20Rik	ankrin repeat domain 50	71670721	99696	XM_130845.5
E4f1	E4F transcription factor 1	1199	13560	NM_007893
E530011N06Rik		77280557		
Ebf4	early B-cell factor 4	71020443	228598	NM_152993.1
Ebpl	emopamil binding protein-like	323392	68177	NM_026598.1
Ece2	endothelin converting enzyme 2	77332686	107522	NM_139293.1
Ecel1	endothelin converting enzyme-like 1	70231305	13599	NM_021306.2
Echdc2	enoyl Coenzyme A hydratase domain containing 2	71836871	52430	NM_026728.1
Edc3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	77414911		NM_153799.1

Edg1	endothelial differentiation sphingolipid G-protein-coupled receptor 1	75043142	13609	NM_007901.3
Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	101289	14745	NM_010336.1
Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	67779874	14745	NM_010336.1
Edg8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	2175	94226	NM_053190
Ednrb	endothelin receptor type B	74750017	13618	NM_007904.2
Eef1a1	eukaryotic translation elongation factor 1 alpha 1	73817934	13627	NM_010106.1
Eef1b2	eukaryotic translation elongation factor 1 beta 2	75934526	55949	NM_018796.2
Eef1g	eukaryotic translation elongation factor 1 gamma	74819238	67160	NM_026007.2
Eef2	eukaryotic translation elongation factor 2	67936204	13629	NM_007907.1
Efcbp1	EF hand calcium binding protein 1	72472791	69352	NM_178617.3
Efcbp2	EF hand calcium binding protein 2	73788010	117148	NM_054095.1
Efcbp2	EF hand calcium binding protein 2	73788011	117148	NM_054095.1
Efemp2	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	2177	58859	NM_021474
Efna1	ephrin A1	1347	13636	NM_010107
Efna3	ephrin A3	381	13638	XM_204001
Efna5	ephrin A5	383	13640	NM_010109
Efnb2	ephrin B2	72079959	13642	NM_010111.2
Efnb3	ephrin B3	387	13643	NM_007911
Egfl5	multiple EGF-like-domains 9	74658078	230316	NM_172694.1
Egfr	epidermal growth factor receptor	1701	13649	NM_007912
Egln1	EGL nine homolog 1 (C. elegans)	77340476	112405	NM_053207.1
Egr1	early growth response 1	71247672	13653	NM_007913.2
Egr2	early growth response 2	72128749	13654	NM_010118.1
Egr3	early growth response 3	74581377	13655	NM_018781.1
Egr4	early growth response 4	74800827	13656	NM_020596.1
Egr4	early growth response 4	73931407	13656	NM_020596.1
Ehd3	EH-domain containing 3	71836903	57440	NM_020578.1
Ehd4	EH-domain containing 4	74275102	98878	NM_133838.2
Ei24	etoposide induced 2.4 mRNA	2179	13663	NM_007915
Eif1ay	eukaryotic translation initiation factor 1A, Y-linked	74988539	66235	NM_025437.2
Eif1b	eukaryotic translation initiation factor 1B	75651231	68969	NM_026892.1
Eif2ak3	eukaryotic translation initiation factor 2 alpha kinase 3	2181	13666	NM_010121
Eif3s1	eukaryotic translation initiation factor 3, subunit J	321196	78655	NM_144545.1
Eif4b	eukaryotic translation initiation factor 4B	355885	75705	NM_145625.1
Eif5a	eukaryotic translation initiation factor 5A	2183	276770	NM_181582
Eif5a2	eukaryotic translation initiation factor 5A2	73992947	208691	NM_177586.4
Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	72340123	15569	NM_010486.2
Elf2	E74-like factor 2	1349	69257	NM_023502
Elk1	ELK1, member of ETS oncogene family	2185	13712	NM_007922
Elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)	70743907	140580	NM_080288.1
Elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)	71015802	140579	NM_080287.2
Elmo3	engulfment and cell motility 3, ced-12 homolog (C. elegans)	73718049	234683	NM_172760.1
Elmod1	ELMO domain containing 1	71924269	270162	NM_177769.2
Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	74882527	54325	NM_019422.1
Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	74273118	68801	NM_134255.2
Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	74425551	170439	NM_130450.1
Emb	embigin	73930836	13723	NM_010330.2
Eml1	echinoderm microtubule associated protein like 1	73992948	68519	XM_127139.6
Emp1	epithelial membrane protein 1	77280421	13730	NM_010128.3

En2	engrailed 2	74988733	13799	NM_010134.1
Enc1	ectodermal-neural cortex 1	390	13803	NM_007930
Eno2	enolase 2, gamma neuronal	82991	13807	NM_013509.2
Enpep	glutamyl aminopeptidase	73769289	13809	NM_007934.1
Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	70613967	18606	NM_015744.1
Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	77413700	18606	NM_015744.1
Enpp6	ectonucleotide pyrophosphatase/phosphodiesterase 6	74882555	320981	NM_177304.2
Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	393	12495	NM_009848
Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	73732144	12496	NM_009849.1
Entpd3	ectonucleoside triphosphate diphosphohydrolase 3	74511804	215446	NM_178676.2
Eomes	eomesodermin homolog (Xenopus laevis)	395	13813	NM_010136
Epb4.111	erythrocyte protein band 4.1-like 1	74047777	13821	XM_487678.1
Epb4.112	erythrocyte protein band 4.1-like 2	70431433	13822	NM_013511.1
Epb4.9	erythrocyte protein band 4.9	398	13829	NM_013514
Epdr2	ependymin related protein 1 (zebrafish)	74881156	105298	NM_134065.2
Epha1	Eph receptor A1	74640882	13835	NM_023580.2
Epha10	Eph receptor A10	73930823	230735	NM_177671.2
Epha3	Eph receptor A3	72472792	13837	NM_010140.1
Epha4	Eph receptor A4	2187	13838	NM_007936
Epha6	Eph receptor A6	72472793	13840	NM_007938.1
Epha7	Eph receptor A7	402	13841	NM_010141
Epha8	Eph receptor A8	72472794	13842	NM_007939.1
Ephb1	Eph receptor B1	72077478	270190	NM_173447.2
Ephb3	Eph receptor B3	1492	13845	NM_010143
Ephb6	Eph receptor B6	2191	13848	NM_007680
Ephx2	epoxide hydrolase 2, cytoplasmic	70813923	13850	NM_007940.2
Epn3	epsin 3	74357584	71889	NM_027984.1
Eps15	epidermal growth factor receptor pathway substrate 15	72080144	13858	NM_007943.1
Eps15-rs	epidermal growth factor receptor pathway substrate 15-like 1	2193		NM_007944
Eps8	epidermal growth factor receptor pathway substrate 8	1705	13860	NM_007945
Eps8l1	EPS8-like 1	1707	67425	NM_026146
Eps8l2	EPS8-like 2	74658244	98845	NM_133191.2
Eps8l3	ESP8-like 3	404	99662	NM_133867
ErbB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	1709	13866	XM_109715
ErbB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	72472797	13869	XM_136682.4
Erdr1	erythroid differentiation regulator 1	378	170942	NM_133362
Erf	Ets2 repressor factor	2195	13875	NM_010155
Erh	enhancer of rudimentary homolog (Drosophila)	2197	13877	NM_007951
Ern2	endoplasmic reticulum (ER) to nucleus signalling 2	72472798	26918	NM_012016.1
Ero1lb	ERO1-like beta (S. cerevisiae)	72340145	67475	NM_026184.2
Erp29	endoplasmic reticulum protein 29	72007751	67397	NM_026129.2
Esr1	estrogen receptor 1 (alpha)	1454	13982	NM_007956
Esr2	estrogen receptor 2 (beta)	71670737	13983	NM_010157.3
Esrra	estrogen related receptor, alpha	1351	26379	NM_007953
Esrrg	estrogen-related receptor gamma	73616033	26381	NM_011935.1
Etfa	electron transferring flavoprotein, alpha polypeptide	74581380	110842	NM_145615.2
Ets1	E26 avian leukemia oncogene 1, 5' domain	2199	23871	NM_011808
Ets2	E26 avian leukemia oncogene 2, 3' domain	1201	23872	NM_011809
Etv1	ets variant gene 1	72119595	14009	NM_007960.1

Etv3	ets variant gene 3	1494	27049	NM_012051
Etv5	ets variant gene 5	70613989	104156	NM_023794.2
Etv6	ets variant gene 6 (TEL oncogene)	1353	14011	NM_007961
Evi5	ecotropic viral integration site 5	71670743	14020	NM_007964.1
Ewsr1	Ewing sarcoma breakpoint region 1	408	14030	NM_007968
Exosc1	exosome component 1	2203	66583	NM_025644
Exosc8	exosome component 8	74658079	69639	NM_027148.2
Extl2	exotoses (multiple)-like 2	70613979	58193	NM_021388.2
Extl3	exostoses (multiple)-like 3	411	54616	NM_018788
Eya1	eyes absent 1 homolog (Drosophila)	73818759	14048	NM_010164.1
Eya2	eyes absent 2 homolog (Drosophila)	70743234	14049	NM_010165.1
Eya4	eyes absent 4 homolog (Drosophila)	77280436	14051	NM_010167.2
F11r	F11 receptor	75773698	16456	NM_172647.1
F13a1	coagulation factor XIII, A1 subunit	74882565	74145	NM_028784.2
F2r	coagulation factor II (thrombin) receptor	1711	14062	NM_010169
F2rl1	coagulation factor II (thrombin) receptor-like 1	199391	14063	NM_007974.2
F3	coagulation factor III	77280341	14066	NM_010171.2
F5	coagulation factor V	73992763	14067	NM_007976.1
F630102L10Rik		75144622		
F830020C16Rik	homeobox containing 1	70301273	219150	NM_177338.3
F930020C14Rik		77280430		
Fa2h	fatty acid 2-hydroxylase	74882584	338521	NM_178086.2
Fabp3	fatty acid binding protein 3, muscle and heart	418	14077	NM_010174
Fabp5	fatty acid binding protein 5, epidermal	70634396	16592	NM_010634.1
Fabp7	fatty acid binding protein 7, brain	72104184	12140	NM_021272.2
Fancd2	Fanconi anemia, complementation group D2	73635979	211651	XM_132796.5
Fasn	fatty acid synthase	74425543	14104	NM_007988.1
Fat4	FAT tumor suppressor homolog 4 (Drosophila)	74363356	329628	XM_619892.1
Fbln1	fibulin 1	2205	14114	NM_010180
Fbln2	fibulin 2	321208	14115	NM_007992.1
Fbn2	fibrillin 2	72472799	14119	NM_010181.1
Fbs1	fibrosin	2207	14123	XM_284344
Fbxl5	F-box and leucine-rich repeat protein 5	422	242960	NM_178729
Fbxo18	F-box protein 18	293462	50755	NM_015792.1
Fbxo2	F-box protein 2	2210	230904	NM_176848
Fbxo21	F-box protein 21	70634119	231670	NM_145564.2
Fbxo34	F-box protein 34	74882585	78938	NM_030236.1
Fbxo44	F-box protein 44	77340498	230903	NM_173401.1
Fbxo9	f-box protein 9	74800954	71538	NM_023605.1
Fbxw2	F-box and WD-40 domain protein 2	355882	30050	NM_013890.2
Fbxw7	F-box and WD-40 domain protein 7, archipelago homolog (Drosophila)	72128750	50754	NM_080428.2
Fdft1	farnesyl diphosphate farnesyl transferase 1	75041432	14137	NM_010191.2
Fdps	farnesyl diphosphate synthetase	76085745	110196	NM_134469.2
Fem1a	feminization 1 homolog a (C. elegans)	2212	14154	NM_010192
Fez2	fasciculation and elongation protein zeta 2 (zygin II)	74272477	225020	NM_199448.1
Fgd3	FYVE, RhoGEF and PH domain containing 3	72472800	30938	NM_015759.1
Fgd5	FYVE, RhoGEF and PH domain containing 5	74357548	232237	NM_172731.2
Fgf1	fibroblast growth factor 1	655498	14164	NM_010197.2
Fgf1	fibroblast growth factor 1	2214	14164	NM_010197

Fgf12	fibroblast growth factor 12	424	14167	NM_010199
Fgf13	fibroblast growth factor 13	427	14168	NM_010200
Fgf15	fibroblast growth factor 15	1715	14170	NM_008003
Fgfr1	fibroblast growth factor receptor 1	440	14182	NM_010206
Fgfr1op2	FGFR1 oncogene partner 2	70743887	67529	NM_026218.1
Fgfr2	fibroblast growth factor receptor 2	445	14183	NM_010207
Fgfr3	fibroblast growth factor receptor 3	448	14184	NM_008010
Fgfr4	fibroblast growth factor receptor 4	1581	14186	NM_008011
Fh1	fumarate hydratase 1	355890	14194	NM_010209.1
Fhl1	four and a half LIM domains 1	2218	14199	NM_010211
Fhl2	four and a half LIM domains 2	70743903	14200	NM_010212.1
FHOS2	formin homology 2 domain containing 3	71924400	225288	NM_175276.3
Fibcd1	fibrinogen C domain containing 1	72472801	98970	NM_178887.2
Fign	fidgetin	72081550	60344	NM_021716.1
Filip1	filamin A interacting protein 1	73635796	70598	XM_486240.1
Fin15	-	73994666	14210	NM_008016.2
Fjx1	four jointed box 1 (Drosophila)	1203	14221	NM_010218
Fkbp10	FK506 binding protein 10	2220	14230	NM_010221
Fkbp6	FK506 binding protein 6	2222	94244	NM_033571
Flcn	folliculin	227163	216805	NM_146018.1
Flot1	flotillin 1	67752111	14251	NM_008027.1
Flot2	flotillin 2	74511805	14252	NM_008028.1
Flrt2	fibronectin leucine rich transmembrane protein 2	73931417	399558	NM_201518.1
Flrt3	fibronectin leucine rich transmembrane protein 3	73931404	71436	NM_178382.2
Flt1	FMS-like tyrosine kinase 1	2224	14254	NM_010228
Flt3l	FMS-like tyrosine kinase 3 ligand	248334	14256	NM_013520.2
Fmn1	formin-like 1	75041433	57778	NM_019679.1
Fmo1	flavin containing monooxygenase 1	72008121	14261	NM_010231.2
Fn1	fibronectin 1	72119593	14268	NM_010233.1
Fndc1	fibronectin type III domain containing 1	73992908	68655	XM_354975.2
Fndc3b	fibronectin type III domain containing 3B	74988759	72007	NM_173182.1
Fndc4	fibronectin type III domain containing 4	293665	64339	NM_022424.2
Fndc5	fibronectin type III domain containing 5	73635989	384061	NM_027402.2
Fnta	farnesyltransferase, CAAX box, alpha	2226	14272	NM_008033
Folr2	folate receptor 2 (fetal)	1717	14276	NM_008035
Fos	FBJ osteosarcoma oncogene	458	14281	NM_010234
Foxa1	forkhead box A1	2228	15375	NM_008259
Foxa1	forkhead box A1	77869794	15375	NM_008259.1
Foxa3	forkhead box A3	1722	15377	NM_008260
Foxb1	forkhead box B1	460	64290	NM_022378
Foxb2	forkhead box B2	1609	14240	NM_008023
Foxd3	forkhead box D3	1496	15221	NM_010425
Foxg1	forkhead box G1	2230	15228	NM_008241
Foxi1	forkhead box I1	2232	14233	NM_023907
Foxo1	forkhead box O1	71249055	56458	NM_019739.2
Foxp1	forkhead box P1	71249056	108655	NM_053202.1
Foxp2	forkhead box P2	72079884	114142	NM_053242.3
Fras1	Fraser syndrome 1 homolog (human)	73994667	231470	NM_175473.2
Frat2	frequently rearranged in advanced T-cell lymphomas 2	1553	212398	NM_177603

Freq	frequenin homolog (Drosophila)	77332082	14299	NM_019681.2
Frmd6	FERM domain containing 6	73931382	319710	NM_028127.3
Frmpd1	FERM and PDZ domain containing 1	73520978	242417	XM_204152.3
Frs3	fibroblast growth factor receptor substrate 3	2234	107971	NM_144939
Frzb	frizzled-related protein	2237	20378	NM_011356
Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	74658080	14086	NM_007984.1
Fst	folliculin	72283811	14313	NM_008046.1
Fstl1	folliculin-like 1	71016596	14314	NM_008047.2
Fstl4	folliculin-like 4	71717187	320027	NM_177059.2
Fstl5	folliculin-like 5	72283812	213262	NM_178673.3
Fthfd	aldehyde dehydrogenase 1 family, member L1	1724		NM_027406
Fts	thymoma viral proto-oncogene 1 interacting protein	1355	14339	NM_010241
Fut8	fucosyltransferase 8	72007749	53618	NM_016893.2
Fxyd5	FXYD domain-containing ion transport regulator 5	74819694	18301	NM_008761.2
Fxyd6	FXYD domain-containing ion transport regulator 6	73592534	59095	NM_022004.5
Fxyd7	FXYD domain-containing ion transport regulator 7	73592536	57780	NM_022007.1
Fyn	Fyn proto-oncogene	70615595	14360	NM_008054.1
Fzd1	frizzled homolog 1 (Drosophila)	2239	14362	NM_021457
Fzd3	frizzled homolog 3 (Drosophila)	466	14365	NM_021458
Fzd4	frizzled homolog 4 (Drosophila)	2241	14366	NM_008055
Fzd4	frizzled homolog 4 (Drosophila)	77925095	14366	NM_008055.2
Fzd5	frizzled homolog 5 (Drosophila)	1500	14367	NM_022721
Fzd6	frizzled homolog 6 (Drosophila)	74047775	14368	NM_008056.2
Fzd6	frizzled homolog 6 (Drosophila)	2243	14368	NM_008056
Fzd8	frizzled homolog 8 (Drosophila)	470	14370	NM_008058
Fzd9	frizzled homolog 9 (Drosophila)	73907498	14371	XM_284144.3
Gaa	glucosidase, alpha, acid	356090	14387	NM_008064.2
Gaa	glucosidase, alpha, acid	77869861	14387	NM_008064.2
Gabarap	gamma-aminobutyric acid receptor associated protein	2245	56486	NM_019749
Gabarapl1	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	654925	57436	NM_020590.3
Gabpb1	GA repeat binding protein, beta 1	121098	14391	NM_010249.1
Gabra1	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	72340131	14394	NM_010250.2
Gabra2	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	74988690	14395	NM_008066.2
Gabra3	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 3	70562043	14396	NM_008067.2
Gabra4	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4	71924402	14397	NM_010251.1
Gabra5	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 5	72077453	110886	NM_176942.2
Gabra6	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 6	75551467	14399	NM_008068.1
Gabrb1	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 1	2247	14400	NM_008069
Gabrb2	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 2	472	14401	NM_008070
Gabrb3	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3	75551468	14402	NM_008071.2
Gabrd	gamma-aminobutyric acid (GABA-A) receptor, subunit delta	76097697	14403	NM_008072.1
Gabrd	gamma-aminobutyric acid (GABA-A) receptor, subunit delta	75551464	14403	NM_008072.1
Gabre	gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon	75749417	14404	NM_017369.1
Gabrg1	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	75551469	14405	NM_010252.3
Gabrg2	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 2	474	14406	NM_008073
Gabrg3	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 3	71587875	14407	NM_008074.1
Gabrp	gamma-aminobutyric acid (GABA-A) receptor, pi	75888749	216643	NM_146017.2
Gabrq	gamma-aminobutyric acid (GABA-A) receptor, subunit theta	73788021	57249	NM_020488.1
Gabrq	gamma-aminobutyric acid (GABA-A) receptor, subunit theta	73788031	57249	NM_020488.1



Gabbr1	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1	75551470	14408	NM_008075.1
Gabbr2	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 2	70436735	14409	NM_008076.2
Gabt4	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	72472802	243616	NM_172890.1
Gad1	glutamic acid decarboxylase 1	69120554	14415	NM_008077.2
Gad1	glutamic acid decarboxylase 1	479	14415	NM_008077
Gad2	glutamic acid decarboxylase 2	481	14417	NM_008078
Gadd45b	growth arrest and DNA-damage-inducible 45 beta	70928374	17873	NM_008655.1
Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	70634407	23882	NM_011817.1
Gal	galanin	70231997	14419	NM_010253.2
Galm	galactose mutarotase	2249	319625	NM_176963
Galns	galactosamine (N-acetyl)-6-sulfate sulfatase	70612726	50917	NM_016722.2
Galnt10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10	70814342	171212	NM_134189.2
Galnt13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13	72472803	271786	NM_173030.1
Galnt14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14	72472804	71685	XM_128787.4
Galnt6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6	74882595	207839	NM_172451.1
Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9	73817422	231605	NM_198306.1
Galntl1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	71717305	108760	XM_283069.3
Galntl4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	70928328	233733	NM_173739.3
Galr1	galanin receptor 1	72283790	14427	NM_008082.1
Gap43	growth associated protein 43	70928270	14432	NM_008083.2
Garnl3	GTPase activating RANGAP domain-like 3	73994668	99326	NM_178888.3
Garnl4	GTPase activating RANGAP domain-like 4	74882606	380711	XM_484050.1
Gas1	growth arrest specific 1	2251	14451	NM_008086
Gas5	growth arrest specific 5	483	14455	NM_013525
Gas6	growth arrest specific 6	72008122	14456	NM_019521.1
Gas7	growth arrest specific 7	73992909	14457	NM_008088.1
Gata2	GATA binding protein 2	485	14461	NM_008090
Gata3	GATA binding protein 3	73931427	14462	NM_008091.2
Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	1205	67092	NM_025961
Gba	glucosidase, beta, acid	1611	14466	NM_008094
Gbas	glioblastoma amplified sequence	74819681	14467	NM_008095.1
Gbe1	glucan (1,4-alpha-), branching enzyme 1	75042250	74185	NM_028803.2
Gbx2	gastrulation brain homeobox 2	488	14472	NM_010262
Gbx2	gastrulation brain homeobox 2	77868786	14472	NM_010262.2
Gcg	glucagon	75749416	14526	NM_008100.2
Gcgr	glucagon receptor	1613	14527	NM_008101
Gch1	GTP cyclohydrolase 1	70813921	14528	NM_008102.2
Gchfr	GTP cyclohydrolase I feedback regulator	74511806	320415	NM_177157.2
Gckr	glucokinase regulatory protein	74274683	231103	NM_144909.1
Gda	guanine deaminase	74047444	14544	NM_010266.1
Gdap10	ganglioside-induced differentiation-associated-protein 10	74357577	14546	NM_010268.1
Gdap11	ganglioside-induced differentiation-associated protein 1-like 1	75774676	228858	NM_144891.1
Gdap2	ganglioside-induced differentiation-associated-protein 2	275871	14547	NM_010269.1
Gdap2	ganglioside-induced differentiation-associated-protein 2	77414567	14547	NM_010269.1
Gdf1	growth differentiation factor 1	75081205	14559	NM_008107.2
Gdf11	growth differentiation factor 11	74272478	14561	XM_125935.3
Gdi3	guanosine diphosphate (GDP) dissociation inhibitor 2	491		NM_008112
Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2	74047789	71584	NM_023608.2
Gem	GTP binding protein (gene overexpressed in skeletal muscle)	73817928	14579	NM_010276.1

Gemin4	gem (nuclear organelle) associated protein 4	74818624	276919	NM_177367.2
Gfap	glial fibrillary acidic protein	1357	14580	NM_010277
Gfpt2	glutamine fructose-6-phosphate transaminase 2	74425526	14584	NM_013529.1
Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	71064217	14585	NM_010279.2
Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	72472805	14586	NM_008115.1
Ggtl3	gamma-glutamyltransferase-like 3	75145998	207182	NM_144786.1
Ghitm	growth hormone inducible transmembrane protein	1207	66092	NM_078478
Ghrh	growth hormone releasing hormone	496	14601	NM_010285
Ghsr	growth hormone secretagogue receptor	74511739	208188	NM_177330.2
Gipc2	GIPC PDZ domain containing family, member 2	74658141	54120	NM_016867.1
Giyd2	GIY-YIG domain containing 2	74819688	75764	NM_029420.1
Gja1	gap junction membrane channel protein alpha 1	2255	14609	NM_010288
Gja7	gap junction membrane channel protein alpha 7	71064139	14615	NM_008122.1
Gja7	gap junction membrane channel protein alpha 7	77887876	14615	NM_008122.1
Gja9	gap junction membrane channel protein alpha 9	71836902	14617	NM_010290.2
Gjb2	gap junction membrane channel protein beta 2	1359	14619	NM_008125
Gjb5	gap junction membrane channel protein beta 5	2259	14622	NM_010291
Gjb6	gap junction membrane channel protein beta 6	2261	14623	NM_008128
Glcc1	glucocorticoid induced transcript 1	74425568	170772	NM_133236.1
Glce	glucuronyl C5-epimerase	74641306	93683	NM_033320.2
Gldc	glycine decarboxylase	74658091	104174	NM_138595.1
Gldc	glycine decarboxylase	77887886	104174	NM_138595.1
Glg1	golgi apparatus protein 1	75042254	20340	NM_009149.1
Gli3	GLI-Kruppel family member GLI3	1615	14634	NM_008130
Glipr1	GLI pathogenesis-related 1 (glioma)	74586665	73690	NM_028608.1
Glo1	glyoxalase 1	74047916	109801	NM_025374.2
Glp1r	glucagon-like peptide 1 receptor	74511737	14652	NM_021332.1
Glr1	glycine receptor, alpha 1 subunit	72108824	14654	NM_020492.2
Glr2	glycine receptor, alpha 2 subunit	73636121	237213	NM_183427.1
Glr3	glycine receptor, alpha 3 subunit	73788474	110304	NM_080438.1
Glr3	glycine receptor, alpha 3 subunit	73788475	110304	NM_080438.1
Glr4	glycine receptor, alpha 4 subunit	75551476	14657	NM_010297.1
Glrb	glycine receptor, beta subunit	498	14658	NM_010298
Glrx1	glutaredoxin	73931409	93692	NM_053108.2
Gls	glutaminase	500	14660	XM_129846
Glud1	glutamate dehydrogenase 1	503	14661	NM_008133
Glul	glutamate-ammonia ligase (glutamine synthetase)	74047918	14645	NM_008131.2
Gm1012	G protein-coupled receptor 176	74511881	381413	NM_201367.1
Gm1052	VGF nerve growth factor inducible	71924165	381677	XM_355651.2
Gm1088		77340470		XM_355919.2
Gm1175	ankyrin-repeat and fibronectin type III domain containing 1	74047714	382543	XM_356556.2
Gm1335	gene model 1335, (NCBI)	74988767	383783	XM_357245.1
Gm1752	gene model 1752, (NCBI)	74658081	385658	XM_358860.2
Gm196		71670725	237234	XM_136166.4
Gm197	achaete-scute complex homolog 5 (Drosophila)	74988285	226439	XM_136181.3
Gm208Gpr	G protein-coupled receptor 161	70562045	240888	XM_136361.3
Gm22	gene model 22, (NCBI)	74988274	195209	XM_111398.5
Gm2a	GM2 ganglioside activator protein	74988549	14667	NM_010299.2
Gm337	dual specificity phosphatase 5	73931633	240672	XM_140740.4

Gm351	leucine rich repeat containing 55	73931406	241528	XM_141031.4
Gm441	zinc finger protein 804B	73931632	207618	XM_144169.2
Gm508	immunoglobulin superfamily, member 9B	75147761	235086	XM_146674.5
Gm519	transmembrane protein 22	74511956	245020	XM_147067.3
Gm528	gene model 528, (NCBI)	74511946	217951	XM_147716.4
Gm573	adherens junction associated protein 1	71717560	230959	XM_149565.4
Gm623	sterile alpha motif domain containing 3	1375	268288	XM_193552
Gm626	FERM and PDZ domain containing 2	73931634	268729	XM_193753.3
Gm687	gene model 687, (NCBI)	71924145	272465	XM_198094.3
Gm78	protocadherin 17	73636095	219228	XM_127786.4
Gm837	thrombospondin, type I, domain containing 7A	71924155	330267	XM_287555.3
Gm937	BAI1-associated protein 3	75081206	545192	TC1428447.1
Gm953	gene model 953, (NCBI)	2419	381163	
Gmfb	glia maturation factor, beta	1726	63985	NM_022023
Gmppa	GDP-mannose pyrophosphorylase A	73818757	69080	NM_133708.1
Gmpr	guanosine monophosphate reductase	74581368	66355	NM_025508.1
Gmps	guanine monphosphate synthetase	1361	229363	XM_130877
Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	72472806	14677	XM_355574.2
Gnai2	guanine nucleotide binding protein, alpha inhibiting 2	2263	14678	NM_008138
Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type	72472807	14680	NM_010307.1
Gnao1	guanine nucleotide binding protein, alpha o	72081553	14681	NM_010308.2
Gnao1	guanine nucleotide binding protein, alpha o	506	14681	NM_010308
Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	509	14683	NM_010309
Gnat1	guanine nucleotide binding protein, alpha transducing 1	2265	14685	NM_008140
Gnaz	guanine nucleotide binding protein, alpha z subunit	1730	14687	NM_010311
Gnb1	guanine nucleotide binding protein, beta 1	61413	14688	NM_008142.2
Gnb2	guanine nucleotide binding protein, beta 2	512	14693	NM_010312
Gnb4	guanine nucleotide binding protein, beta 4	74047771	14696	NM_013531.2
Gnb5	guanine nucleotide binding protein, beta 5	1456	14697	NM_010313
Gng11	guanine nucleotide binding protein (G protein), gamma 11	1732	66066	NM_025331
Gng12	guanine nucleotide binding protein (G protein), gamma 12	72080065	14701	NM_025278.2
Gng13	guanine nucleotide binding protein 13, gamma	73615561	64337	NM_022422.3
Gng2	guanine nucleotide binding protein (G protein), gamma 2 subunit	67936006	14702	NM_010315.2
Gng2	guanine nucleotide binding protein (G protein), gamma 2 subunit	77414160	14702	NM_010315.2
Gng3	guanine nucleotide binding protein (G protein), gamma 3 subunit	1209	14704	NM_010316
Gng4	guanine nucleotide binding protein (G protein), gamma 4 subunit	515	14706	NM_010317
Gng7	guanine nucleotide binding protein (G protein), gamma 7 subunit	1734	14708	NM_010319
Gng7	guanine nucleotide binding protein (G protein), gamma 7 subunit	77371857	14708	NM_010319.2
Gnpnat1	glucosamine-phosphate N-acetyltransferase 1	2267	54342	NM_019425
Gnrh1	gonadotropin releasing hormone 1	75080152	14714	NM_008145.1
GnT-IX	mannoside acetylglucosaminyltransferase 5, isoenzyme B	73616036	268510	NM_172948.2
Gosr2	golgi SNAP receptor complex member 2	67855413	56494	NM_019650.2
Got2	glutamate oxaloacetate transaminase 2, mitochondrial	76115728	14719	NM_010325.1
Gpc1	glypican 1	73994669	14733	NM_016696.1
Gpc2	glypican 2 (cerebroglycan)	72472808	71951	NM_172412.1
Gpc3	glypican 3	71020431	14734	NM_016697.2
Gpc4	glypican 4	1617	14735	NM_008150
Gpc5	glypican 5	74047712	103978	NM_175500.2
Gpc6	glypican 6	1736	23888	NM_011821

Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	74586667	14555	NM_010271.2
Gpd1l	glycerol-3-phosphate dehydrogenase 1-like	74988763	333433	NM_175380.3
Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	70615598	14571	NM_010274.2
Gphn	gephyrin	1211	268566	NM_172952
Gpm6b	glycoprotein m6b	544520	14758	NM_023122.1
Gpnmb	glycoprotein (transmembrane) nmb	74581367	93695	NM_053110.2
Gpr10	prolactin releasing hormone receptor	74511758	226278	NM_201615.1
Gpr101	G protein-coupled receptor 101	72008495	245424	XM_141764.4
Gpr101	G protein-coupled receptor 101	1213	245424	XM_141764
Gpr103	G protein-coupled receptor 103	71717619	229214	NM_198192.1
Gpr108	G protein-coupled receptor 108	1619	78308	NM_030084
Gpr115	G protein-coupled receptor 115	71587931	78249	XM_128679.3
Gpr116	G protein-coupled receptor 116	73907496	224792	XM_283438.3
Gpr12	G-protein coupled receptor 12	73817425	14738	NM_008151.2
Gpr123	G protein-coupled receptor 123	71924056	52389	XM_486019.1
Gpr125	G protein-coupled receptor 125	74988700	70693	XM_132089.3
Gpr126	G protein-coupled receptor 126	73520982	215798	NM_001002268.1
Gpr133	G protein-coupled receptor 133	74511759	243277	XM_485685.1
Gpr137	G protein-coupled receptor 137	75651149	107173	NM_207220.1
Gpr139	G protein-coupled receptor 139	76097698	209776	XM_146103.2
Gpr139	G protein-coupled receptor 139	77332084	209776	XM_146103.2
Gpr146	G protein-coupled receptor 146	2059	80290	NM_030258
Gpr146	G protein-coupled receptor 146	77371845	80290	NM_030258.2
Gpr151	G protein-coupled receptor 151	74724649	240239	NM_181543.1
Gpr153	G protein-coupled receptor 153	1950	100129	NM_178406
Gpr155	G protein-coupled receptor 155	70562055	68526	XM_130346.4
Gpr156	G protein-coupled receptor 156	74641322	239845	NM_153394.2
Gpr162	G protein-coupled receptor 162	74658160	14788	NM_013533.2
Gpr17	G protein-coupled receptor 17	74641313	574402	NM_001025381.1
Gpr171	G protein-coupled receptor 171	72007564	229323	NM_173398.1
Gpr171	G protein-coupled receptor 171	1713	229323	NM_173398
Gpr172b	G protein-coupled receptor 172B	71016711	52710	NM_029643.2
Gpr173	G-protein coupled receptor 173	74724531	70771	NM_027543.2
Gpr18	G protein-coupled receptor 18	71015809	110168	NM_182806.1
Gpr2	chemokine (C-C motif) receptor 10	74724659	12777	NM_007721.3
Gpr26	G protein-coupled receptor 26	70562057	233919	NM_173410.1
Gpr3	G-protein coupled receptor 3	74511769	14748	NM_008154.1
Gpr35	G protein-coupled receptor 35	293673	64095	NM_022320.2
Gpr37	G protein-coupled receptor 37	2271	14763	NM_010338
Gpr37l1	G protein-coupled receptor 37-like 1	74724670	171469	NM_134438.1
Gpr4	G protein-coupled receptor 4	74724680	319197	NM_175668.2
Gpr50	G-protein-coupled receptor 50	74511770	14765	NM_010340.1
Gpr51	gamma-aminobutyric acid (GABA) B receptor 2	71247614	242425	XM_143750.4
Gpr54	KISS1 receptor	2273		NM_053244
Gpr56	G protein-coupled receptor 56	71015815	14766	NM_018882.2
Gpr6	G protein-coupled receptor 6	71247615	140741	NM_199058.1
Gpr73	prokineticin receptor 1	74724728	58182	NM_021381.3
Gpr73l1	prokineticin receptor 2	74511780	246313	NM_144944.2
Gpr74	neuropeptide FF receptor 2	70562070	104443	NM_133192.2

Gpr83	G protein-coupled receptor 83	72338696	14608	NM_010287.1
Gpr84	G protein-coupled receptor 84	1583	80910	NM_030720
Gpr85	G protein-coupled receptor 85	1738	64450	NM_145066
Gpr88	G-protein coupled receptor 88	519	64378	NM_022427
Gpr89	G protein-coupled receptor 89	67881554	67549	NM_026229.1
Gprc5a	G protein-coupled receptor, family C, group 5, member A	77414145	232431	NM_181444.3
Gprc5b	G protein-coupled receptor, family C, group 5, member B	71836881	64297	NM_022420.1
Gprin1	G protein-regulated inducer of neurite outgrowth 1	75077243	26913	NM_012014.1
Gprk5	G protein-coupled receptor kinase 5	1621	14773	NM_018869
Gprk5	G protein-coupled receptor kinase 5	77371851	14773	NM_018869.2
Gpsn2	glycoprotein, synaptic 2	544902	106529	NM_134118.1
Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	1657	108682	NM_173866
Gpx2	glutathione peroxidase 2	74819652	14776	NM_030677.1
Gpx3	glutathione peroxidase 3	75080750	14778	NM_008161.1
Grb10	growth factor receptor bound protein 10	522	14783	NM_010345
Grb14	growth factor receptor bound protein 14	73997150	50915	NM_016719.1
Grb7	growth factor receptor bound protein 7	1502	14786	NM_010346
Greb1	gene regulated by estrogen in breast cancer protein	71924412	268527	NM_015764.1
Grem2	gremlin 2 homolog, cysteine knot superfamily ( <i>Xenopus laevis</i> )	73992910	23893	NM_011825.1
Gria1	glutamate receptor, ionotropic, AMPA1 (alpha 1)	524	14799	NM_008165
Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2)	75551462	14800	NM_013540.1
Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	71247616	53623	NM_016886.1
Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	71358628	14802	NM_019691.2
Grid1	glutamate receptor, ionotropic, delta 1	74724739	14803	NM_008166.1
Grid2	glutamate receptor, ionotropic, delta 2	71247617	14804	NM_008167.1
Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	71670479	170935	NM_133355.1
GRik	glutamate receptor, ionotropic, kainate 1	75749751	14805	NM_146072.1
GRik	glutamate receptor, ionotropic, kainate 2 (beta 2)	71247618	14806	NM_010349.1
GRik	glutamate receptor, ionotropic, kainate 3	75749418	14807	AF245444.1
GRik	glutamate receptor, ionotropic, kainate 5 (gamma 2)	75551459	14809	NM_008168.1
GRik	glutamate receptor, ionotropic, kainate 4	75551478	110637	NM_175481.2
GRik	glutamate receptor, ionotropic, kainate 1	527		NM_146072
Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)	1585	14810	NM_008169
Grin2a	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	75081000	14811	NM_008170.2
Grin2b	glutamate receptor, ionotropic, NMDA2B (epsilon 2)	74988710	14812	NM_008171.2
Grin2c	glutamate receptor, ionotropic, NMDA2C (epsilon 3)	75888748	14813	NM_010350.1
Grin2d	glutamate receptor, ionotropic, NMDA2D (epsilon 4)	75551479	14814	NM_008172.1
Grin3a	glutamate receptor ionotropic, NMDA3A	73907499	242443	XM_205495.2
Grin3b	glutamate receptor, ionotropic, NMDA3B	535	170483	NM_130455
Grin3b	glutamate receptor, ionotropic, NMDA3B	77869800	170483	NM_130455.1
Grina	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	1948	66168	NM_023168
Grin1a	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	1740	28015	NM_178602
Grip1	glutamate receptor interacting protein 1	74988749	74053	NM_028736.1
Grip2	glutamate receptor interacting protein 2	75651127	243547	XM_144901.5
Grip2	glutamate receptor interacting protein 2	74750053	243547	XM_144901.5
Grm1	glutamate receptor, metabotropic 1	537	14816	NM_016976
Grm3	glutamate receptor, metabotropic 3	539	108069	NM_181850
Grm4	glutamate receptor, metabotropic 4	71247631	268934	XM_196179.3
Grm5	glutamate receptor, metabotropic 5	73512423	108071	XM_149971.4

Grm8	glutamate receptor, metabotropic 8	73771227	14823	NM_008174.1
Grm8	glutamate receptor, metabotropic 8	73771230	14823	NM_008174.1
Grn	granulin	77371839	14824	NM_008175.2
Grp	gastrin releasing peptide	1363	225642	NM_175012
Grp58	protein disulfide isomerase associated 3	71015817	14827	NM_007952.1
Grsf1	G-rich RNA sequence binding factor 1	73994670	231413	NM_178700.2
Gsbs	G substrate	73817988	19051	NM_011153.2
Gsn	gelsolin	72081395	227753	NM_146120.2
Gss	glutathione synthetase	74273307	14854	NM_008180.1
Gsta4	glutathione S-transferase, alpha 4	77278951	14860	NM_010357.1
Gstk1	glutathione S-transferase kappa 1	72129245	76263	NM_029555.1
Gstm4	glutathione S-transferase, mu 4	70743872	14865	NM_026764.2
Gsto1	glutathione S-transferase omega 1	74511807	14873	NM_010362.1
Gtdc1	glycosyltransferase-like domain containing 1	74425541	227835	NM_172662.1
Gtf2f1	general transcription factor IIF, polypeptide 1	67870080	98053	NM_133801.1
Gtf2h2	general transcription factor II H, polypeptide 2	70634256	23894	NM_022011.2
Gtf2h4	general transcription factor II H, polypeptide 4	1458	14885	NM_010364
Gtf2i	general transcription factor II I	2277	14886	NM_010365
Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	7	71752	NM_027901
Gucy1a3	guanylate cyclase 1, soluble, alpha 3	543	60596	NM_021896
Gucy1a3	guanylate cyclase 1, soluble, alpha 3	77866848	60596	NM_021896.3
Gucy2c	guanylate cyclase 2c	73992911	14917	XM_132928.3
Gucy2f	guanylate cyclase 2f	74640883	245650	NM_001007576.1
Guk1	guanylate kinase 1	2279	14923	NM_008193
Gyg1	glycogenin	73817930	27357	NM_013755.1
H2-Eb1	histocompatibility 2, class II antigen E beta	73520983	14969	NM_010382.1
H2-T23	histocompatibility 2, T region locus 23	75749388	15040	NM_010398.1
Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional)	76115729	231086	NM_145558.1
Haghl	hydroxyacylglutathione hydrolase-like	75259440	68977	NM_026897.1
Hap1	huntingtin-associated protein 1	72007561	15114	NM_010404.2
Hap1	huntingtin-associated protein 1	552	15114	NM_010404
Hap1	huntingtin-associated protein 1	549	15114	NM_010404
Hapln1	hyaluronan and proteoglycan link protein 1	77332706	12950	NM_013500.3
Hapln4	hyaluronan and proteoglycan link protein 4	71717078	330790	NM_177900.3
Hars	histidyl-tRNA synthetase	554	15115	NM_008214
Hars2	histidyl-tRNA synthetase 2, mitochondrial (putative)	1742	66044	NM_025314
Hba-a1	hemoglobin alpha, adult chain 1	77332708	15122	NM_008218.1
Hbb	hemoglobin beta chain complex	77340464	15127	XM_489729.1
Hbb-b1	hemoglobin, beta adult major chain	67936011	15129	NM_008220.2
Hbb-b2	hemoglobin, beta adult minor chain	77371773	15127	NM_016956.2
Hc	hemolytic complement	73992912	15139	NM_010406.1
Hcn1	hyperpolarization-activated, cyclic nucleotide-gated K+ 1	77280561	15165	NM_010408.1
Hcn2	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	73512185	15166	NM_008226.1
Hcrt	hypocretin	2283	15171	NM_010410
Hcrtr1	hypocretin (orexin) receptor 1	1215	230777	NM_198959
Hcrtr1	hypocretin (orexin) receptor 1	77868713	230777	NM_198959.1
Hcrtr2	hypocretin (orexin) receptor 2	1395	57781	NM_198962
Hdac6	histone deacetylase 6	74819462	15185	NM_010413.2
Hdac7a	histone deacetylase 7A	75077262	56233	NM_019572.2

Hdc	histidine decarboxylase	71016663	15186	NM_008230.4
Hdgf	hepatoma-derived growth factor	2285	15191	NM_008231
Hdlbp	high density lipoprotein (HDL) binding protein	74819232	110611	NM_133808.2
Hebp1	heme binding protein 1	74988456	15199	NM_013546.1
Hectd1	HECT domain containing 1	357092	207304	XM_283061.2
Hectd2	HECT domain containing 2	2002	226098	NM_172637
Hecw1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	74882685	94253	XM_484217.1
Heg1	HEG homolog 1 (zebrafish)	74958616	77446	NM_175256.4
Hes1	hairy and enhancer of split 1 (Drosophila)	556	15205	NM_008235
Hes3	hairy and enhancer of split 3 (Drosophila)	2287	15207	NM_008237
Hes6	hairy and enhancer of split 6 (Drosophila)	1504	55927	NM_019479
Hes7	hairy and enhancer of split 7 (Drosophila)	2289	84653	NM_033041
Hexb	hexosaminidase B	77340466	15212	NM_010422.1
Hexim1	hexamethylene bis-acetamide inducible 1	74273119	192231	NM_138753.1
Hgf	hepatocyte growth factor	558	15234	NM_010427
Hgf	hepatocyte growth factor	77867710		NM_010427.2
Hhip	Hedgehog-interacting protein	71358556	15245	NM_020259.3
Hiatl1	hippocampus abundant transcript-like 1	77414177	66631	NM_133680.2
Hig1	huntingtin interacting protein 1	2291	215114	NM_019814
Hint1	histidine triad nucleotide binding protein 1	73520984	15254	NM_008248.1
Hip1	huntingtin interacting protein 1	2293	319181	NM_146001
Hip2	huntingtin interacting protein 2	73817935	53323	NM_016786.2
Hist1h1a	histone cluster 1, H1a	74988764	80838	NM_030609.1
Hist1h1b	histone cluster 1, H1b	74272040	56702	NM_020034.1
Hist1h2bc	histone cluster 1, H2bc	560	319179	NM_023422
Hist1h2bg	histone cluster 1, H2bg	73769308	319181	NM_178196.2
Hist2h2aa1	histone cluster 2, H2aa1	72129296	15267	NM_013549.1
Hist3h2a	histone cluster 3, H2a	74583150	319162	NM_178218.2
Hkr2	zinc finger and SCAN domain containing 22	247974	232878	NM_001001447.1
Hkr3	histone cluster 1, H2bc	1940	68024	NM_133879
Hlf	hepatic leukemia factor	565	100090	NM_172563
Hmg20a	high mobility group 20A	357093	66867	NM_025812.2
Hmga1	high mobility group AT-hook 1	2295	217082	NM_016660
Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	75079789	15357	XM_127496.6
Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	1744	15361	NM_145942
Hmox2	heme oxygenase (decycling) 2	75774681	15369	NM_010443.1
Hmx3	H6 homeo box 3	74641309	15373	NM_008257.2
Hnf4a	hepatic nuclear factor 4, alpha	1746	208715	NM_008261
Hnrpd1	heterogeneous nuclear ribonucleoprotein D-like	571	15378	NM_016690
Hnrph2	heterogeneous nuclear ribonucleoprotein H2	61001	56258	NM_019868.2
Hnrph2	heterogeneous nuclear ribonucleoprotein H2	77869111	50926	NM_019868.2
Hnt	neurotrimin	573	56258	NM_172290
Hnt	neurotrimin	77866868	235106	NM_172290.2
Hod	HOP homeobox	2297	74318	NM_175606
Homer1	homer homolog 1 (Drosophila)	1748	26556	NM_011982
Homer2	homer homolog 2 (Drosophila)	71015814	26557	XM_133550.5
Homer3	homer homolog 3 (Drosophila)	356087	26558	NM_011984.1
Hook3	hook homolog 3 (Drosophila)	1197	320191	NM_207659
Hoxa5	homeo box A5	544903	15402	NM_010453.2

Hoxb13	homeo box B13	2299	15408	NM_008267
Hoxd9	homeo box D9	1623	15438	NM_013555
Hpca	hippocalcin	72129291	15444	NM_010471.2
Hpcal1	hippocalcin-like 1	74581395	53602	NM_016677.1
Hpcal4	hippocalcin-like 4	73520985	170638	NM_174998.1
Hpd	4-hydroxyphenylpyruvic acid dioxygenase	75774666	15445	NM_008277.1
Hpd	4-hydroxyphenylpyruvic acid dioxygenase	356492	15445	NM_008277.1
Hpse	heparanase	77340468	15442	NM_152803.2
Hrasls3	HRAS like suppressor 3	2301	225845	NM_139269
Hrh1	histamine receptor H 1	72283792	15465	NM_008285.2
Hrh2	histamine receptor H 2	74724750	15466	NM_008286.1
Hrh3	histamine receptor H 3	73636034	99296	NM_133849.1
Hrmt111	protein arginine N-methyltransferase 2	577		NM_133182
Hs1bp1	HCLS1 associated X-1	2303		NM_011826
Hs3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	2305	15476	NM_010474
Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	74988765	195646	XM_112440.2
Hs6st1	heparan sulfate 6-O-sulfotransferase 1	74819258	50785	NM_015818.1
Hs6st2	heparan sulfate 6-O-sulfotransferase 2	72129255	50786	NM_015819.1
Hs6st3	heparan sulfate 6-O-sulfotransferase 3	73520986	50787	NM_015820.1
Hsbp1	heat shock factor binding protein 1	74581381	68196	NM_024219.1
Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	73520987	15483	NM_008288.1
Hsd12	hydroxysteroid dehydrogenase like 2	74047906	72479	NM_024255.1
Hsf1	heat shock factor 1	67810538	15499	NM_008296.1
Hspa12a	heat shock protein 12A	74047899	73442	NM_175199.1
Hspa1l	heat shock protein 1-like	75041442	15482	NM_013558.1
Hspa4l	heat shock protein 4 like	75749390	18415	NM_011020.3
Hspa5bp1	transmembrane protein 132A	70436749	98170	NM_133804.1
Hspb1	heat shock protein 1	74363357	15507	NM_013560.1
Hspb3	heat shock protein 3	73520988	56534	NM_019960.1
Hspb6	heat shock protein, alpha-crystallin-related, B6	74882616	243912	XM_145511.5
Hspb7	heat shock protein family, member 7 (cardiovascular)	579	29818	NM_013868
Hspb8	heat shock protein 8	1181	80888	NM_030704
Hspb8	heat shock protein 8	77866850	80888	NM_030704.1
Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	581	15550	NM_008308
Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	584	15551	NM_010482
Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	1627	15558	NM_172812
Htr2b	5-hydroxytryptamine (serotonin) receptor 2B	67862429	15559	NM_008311.1
Htr2c	5-hydroxytryptamine (serotonin) receptor 2C	73636098	15560	NM_008312.2
Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	74724760	15561	NM_013561.1
Htr3b	5-hydroxytryptamine (serotonin) receptor 3B	74641318	57014	NM_020274.2
Htr4	5 hydroxytryptamine (serotonin) receptor 4	72119658	15562	NM_008313.1
Htr5b	5-hydroxytryptamine (serotonin) receptor 5B	71247644	15564	NM_010483.2
Hunk	hormonally upregulated Neu-associated kinase	2307	26559	NM_015755
Iars2	isoleucine-tRNA synthetase 2, mitochondrial	74958491	381314	NM_198653.1
Ibrdc2	ring finger protein 144B	71836839	218215	NM_146042.2
Ica1	islet cell autoantigen 1	75988482	15893	NM_010492.2
Ica1	islet cell autoantigen 1	2309	15893	NM_010492
Icam5	intercellular adhesion molecule 5, telencephalin	73520989	15898	NM_008319.1
Icmt	isoprenylcysteine carboxyl methyltransferase	585	57295	NM_133788



Icosl	icos ligand	1217	50723	NM_015790
ICRFP703B1614Q5.5	cDNA sequence BC051019	1558	57355	NM_020609
Id2	inhibitor of DNA binding 2	71836806	15902	NM_010496.2
Id3	inhibitor of DNA binding 3	74724763	15903	NM_008321.1
Id4	inhibitor of DNA binding 4	74357547	15904	NM_031166.1
Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	74511808	15926	NM_010497.1
Ids	iduronate 2-sulfatase	73994671	15931	NM_010498.1
Ier2	immediate early response 2	71836849	15936	NM_010499.2
Ier3	immediate early response 3	72008119	15937	NM_133662.1
Ier5	immediate early response 5	73931410	15939	NM_010500.1
Ifi205	interferon activated gene 205	75079787	226695	NM_172648.2
Ifit2	interferon-induced protein with tetratricopeptide repeats 2	74988457	15958	NM_008332.2
Ifit3	interferon-induced protein with tetratricopeptide repeats 3	74047911	15959	NM_010501.1
Ifnar1	interferon (alpha and beta) receptor 1	588	15975	NM_010508
Ifngr2	interferon gamma receptor 2	1460	15980	NM_008338
Igf2	insulin-like growth factor 2	2313	16002	NM_010514
Igfbp3	insulin-like growth factor binding protein 3	74272920	16009	NM_008343.1
Igfbp4	insulin-like growth factor binding protein 4	71924311	16010	NM_010517.2
Igfbp5	insulin-like growth factor binding protein 5	73592530	16011	NM_010518.1
Igfbp6	insulin-like growth factor binding protein 6	70928248	16012	NM_008344.1
Igfbpl1	insulin-like growth factor binding protein-like 1	1974	75426	NM_018741
Igk-V28	immunoglobulin kappa chain variable 28 (V28)	73732153	16114	XM_132633.5
Igsf11	immunoglobulin superfamily, member 11	72103820	207683	NM_170599.2
Igsf21	immunoglobulin superfamily, member 21	74357578	230868	NM_198610.1
Igsf3	immunoglobulin superfamily, member 3	72081517	78908	NM_207205.1
Igsf4d	cell adhesion molecule 2	73635999	239857	NM_178721.2
Ikbkb	inhibitor of kappaB kinase beta	1750	16150	NM_010546
Il10ra	interleukin 10 receptor, alpha	75041443	16154	NM_008348.1
Il11ra1	interleukin 11 receptor, alpha chain 1	2315	16157	NM_010549
Il11ra2	interleukin 11 receptor, alpha chain 2	75041444	16158	NM_010550.2
Il13ra1	interleukin 13 receptor, alpha 1	74819256	16164	NM_133990.3
Il16	interleukin 16	71064290	16170	NM_010551.1
Il17r	interleukin 17 receptor A	73520990	16172	NM_008359.1
Il17rb	interleukin 17 receptor B	2317	50905	NM_019583
Il17rc	interleukin 17 receptor C	2319	171095	NM_134159
Il1rap	interleukin 1 receptor accessory protein	1462	16180	NM_008364
Il1rapl2	interleukin 1 receptor accessory protein-like 2	73994672	60367	NM_030688.1
Il31ra	interleukin 31 receptor A	74881366	218624	NM_139299.1
Il4ra	interleukin 4 receptor, alpha	119507	16190	NM_010557.1
Il4ra	interleukin 4 receptor, alpha	77413692	16190	NM_010557.1
Ilf3	interleukin enhancer binding factor 3	74425549	16201	NM_010561.1
Impa1	inositol (myo)-1(or 4)-monophosphatase 1	74641325	55980	NM_018864.3
Impact	imprinted and ancient	594	16210	NM_008378
Impg1	interphotoreceptor matrix proteoglycan 1	2321	63859	NM_022016
Impg2	interphotoreceptor matrix proteoglycan 2	74819536	224224	NM_174876.3
Ina	internexin neuronal intermediate filament protein, alpha	71836833	226180	NM_146100.2
Ing4	inhibitor of growth family, member 4	357097	28019	NM_133345.1
Inhba	inhibin beta-A	70431432	16323	NM_008380.1
Inhbb	inhibin beta-B	73636087	16324	XM_148966.5

Inpp1	inositol polyphosphate-1-phosphatase	67870434	16329	NM_008384.1
Inpp4b	inositol polyphosphate-4-phosphatase, type II	72080054	234515	XM_134427.4
Inpp5a	inositol polyphosphate-5-phosphatase A	73994713	212111	NM_183144.1
Insig1	insulin induced gene 1	75041453	231070	NM_153526.2
Insrr	insulin receptor-related receptor	71670480	23920	NM_011832.1
Ipo4	importin 4	74658174	75751	NM_024267.4
Iqsec1	IQ motif and Sec7 domain 1	77332673	232227	NM_182784.1
Iqsec3	IQ motif and Sec7 domain 3	73636153	243621	XM_145005.2
Irak1	interleukin-1 receptor-associated kinase 1	2323	16179	NM_008363
Irs2	insulin receptor substrate 2	74363343	384783	XM_357863.2
Irs4	insulin receptor substrate 4	71717079	16370	NM_010572.1
Irx1	Iroquois related homeobox 1 (Drosophila)	2325	16371	NM_010573
Irx2	Iroquois related homeobox 2 (Drosophila)	1752	16372	NM_010574
Isgf3g	interferon regulatory factor 9	2329	16391	NM_008394
Isl1	ISL1 transcription factor, LIM/homeodomain	596	16392	NM_021459
Isoc1	isochorismatase domain containing 1	73732145	66307	NM_025478.2
Isyna1	myo-inositol 1-phosphate synthase A1	75145997	71780	NM_023627.1
Itga11	integrin, alpha 11	74882626	319480	NM_176922.4
Itga3	integrin alpha 3	598	16400	NM_013565
Itga5	integrin alpha 5 (fibronectin receptor alpha)	74882636	16402	NM_010577.2
Itga7	integrin alpha 7	73520991	16404	NM_008398.1
Itgav	integrin alpha V	74658082	16410	NM_008402.1
Itgb1	integrin beta 1 (fibronectin receptor beta)	76115730	16412	NM_010578.1
Itgb1bp1	integrin beta 1 binding protein 1	71015806	16413	NM_008403.2
Itgb5	integrin beta 5	71920512	16419	NM_010580.1
Itgb8	integrin beta 8	73931631	320910	XM_484197.1
Itgbl1	integrin, beta-like 1	74988458	223272	NM_145467.1
Itih3	inter-alpha trypsin inhibitor, heavy chain 3	600	16426	NM_008407
Itn2a	integral membrane protein 2A	74881146	16431	NM_008409.2
Itn2c	integral membrane protein 2C	67936207	64294	NM_022417.1
Itn2c	integral membrane protein 2C	77414652	64294	NM_022417.1
Itpk1	inositol 1,3,4-triphosphate 5/6 kinase	71923998	217837	NM_172584.1
Itpka	inositol 1,4,5-trisphosphate 3-kinase A	70743897	228550	NM_146125.1
Itpkb	inositol 1,4,5-trisphosphate 3-kinase B	73520992	320404	XM_205854.4
Itp1	inositol 1,4,5-triphosphate receptor 1	72119596	16438	NM_010585.2
Itp3	inositol 1,4,5-triphosphate receptor 3	74047776	16440	XM_484617.1
Itn1	intersectin 1 (SH3 domain protein 1A)	1365	16443	NM_010587
Ivns1abp	influenza virus NS1A binding protein	70813898	117198	NM_028582.2
Jak1	Janus kinase 1	74581365	16451	NM_146145.1
Jam2	junction adhesion molecule 2	602	67374	NM_023844
Jam4	immunoglobulin superfamily, member 5	592	72058	NM_028078
Jarid2	jumonji, AT rich interactive domain 2	604	16468	NM_021878
Jmjd2b	jumonji domain containing 2B	2331	193796	NM_172132
Jun	Jun oncogene	2333	16476	NM_010591
Junb	Jun-B oncogene	2335	16477	NM_008416
Jund1	Jun proto-oncogene related gene d	606	16478	NM_010592
Jundm2	Jun dimerization protein 2	73930842	81703	NM_030887.2
Jup	junction plakoglobin	74425547	16480	NM_010593.1
Kb36	keratin 73	74750042	223915	NM_212485.1

Kbtbd3	kelch repeat and BTB (POZ) domain containing 3	74988611	69149	NM_026962.1
Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1	73994714	16485	NM_010595.2
Kcna2	potassium voltage-gated channel, shaker-related subfamily, member 2	75038432	16490	NM_008417.2
Kcna6	potassium voltage-gated channel, shaker-related, subfamily, member 6	74819554	16494	NM_013568.3
Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	70301087	16497	NM_010597.2
Kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	1754	16498	NM_010598
Kcnab3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	73817925	16499	NM_010599.2
Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1	74047856	16500	NM_008420.3
Kcnb2	potassium voltage gated channel, Shab-related subfamily, member 2	74581424	98741	XM_136482.3
Kcnc1	potassium voltage gated channel, Shaw-related subfamily, member 1	72108825	16502	NM_008421.1
Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	75147765	268345	XM_193580.4
Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	71670481	16504	NM_008422.1
Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	1756	99738	NM_145922
Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	71020432	16508	NM_019697.3
Kcnd3	potassium voltage-gated channel, Shal-related family, member 3	75147766	56543	NM_019931.1
Kcne2	potassium voltage-gated channel, Isk-related subfamily, gene 2	1758	246133	NM_134110
Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3	2337	57442	NM_020574
Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3	77371863	57442	NM_020574.3
Kcne4	potassium voltage-gated channel, Isk-related subfamily, gene 4	74819245	57814	NM_021342.1
Kcnf1	potassium voltage-gated channel, subfamily F, member 1	71358578	382571	NM_201531.1
Kcng3	potassium voltage-gated channel, subfamily G, member 3	71717451	225030	NM_153512.1
Kcng4	potassium voltage-gated channel, subfamily G, member 4	72081560	66733	NM_025734.2
Kcnh1	potassium voltage-gated channel, subfamily H (eag-related), member 1	73636099	16510	NM_010600.1
Kcnh3	potassium voltage-gated channel, subfamily H (eag-related), member 3	74641310	16512	NM_010601.2
Kcnh7	potassium voltage-gated channel, subfamily H (eag-related), member 7	70562103	170738	NM_133207.1
Kcnh8	potassium voltage-gated channel, subfamily H (eag-related), member 8	70562113	211468	XM_140016.5
Kcnip1	Kv channel-interacting protein 1	1760	70357	NM_027398
Kcnip4	Kv channel interacting protein 4	71924387	80334	NM_030265.2
Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	74882646	16515	NM_010603.3
Kcnj14	potassium inwardly-rectifying channel, subfamily J, member 14	67853369	211480	NM_145963.1
Kcnj14	potassium inwardly-rectifying channel, subfamily J, member 14	75651203	211480	NM_145963.1
Kcnj15	potassium inwardly-rectifying channel, subfamily J, member 15	2339	16516	NM_019664
Kcnj16	potassium inwardly-rectifying channel, subfamily J, member 16	2341	16517	NM_010604
Kcnj2	potassium inwardly-rectifying channel, subfamily J, member 2	73636088	16518	NM_008425.2
Kcnj2	potassium inwardly-rectifying channel, subfamily J, member 2	77874598	16518	NM_008425.2
Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	72340132	16519	NM_008426.1
Kcnj4	potassium inwardly-rectifying channel, subfamily J, member 4	74357568	16520	NM_008427.2
Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	72119660	16521	NM_010605.2
Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	609	16522	NM_010606
Kcnj8	potassium inwardly-rectifying channel, subfamily J, member 8	2343	16523	NM_008428
Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	72119580	16524	NM_008429.1
Kcnk1	potassium channel, subfamily K, member 1	67850952	16525	NM_008430.1
Kcnk13	potassium channel, subfamily K, member 13	1762	217826	NM_146037
Kcnk2	potassium channel, subfamily K, member 2	75147764	16526	NM_010607.1
Kcnmb4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	72283793	58802	NM_021452.1
Kcnn2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	77371815	140492	NM_080465.1
Kcnn4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	130911	16534	NM_008433.2
Kcnq3	potassium voltage-gated channel, subfamily Q, member 3	70562114	110862	NM_152923.1
Kcnq4	potassium voltage-gated channel, subfamily Q, member 4	73635775	60613	XM_143960.4

Kcnq5	potassium voltage-gated channel, subfamily Q, member 5	72128745	226922	XM_129704.5
Kcns2	K+ voltage-gated channel, subfamily S, 2	71924259	16539	NM_008436.1
Kcns3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	77371817	238076	NM_173417.1
Kcnv2	potassium channel, subfamily V, member 2	1764	240595	NM_183179
Kctd1	potassium channel tetramerisation domain containing 1	70744515	106931	XM_355081.2
Kctd12	potassium channel tetramerisation domain containing 12	73520993	239217	NM_177715.3
Kctd16	potassium channel tetramerisation domain containing 16	73636009	383348	XM_356997.2
Kctd17	potassium channel tetramerisation domain containing 17	72340180	72844	XM_110121.5
Kctd4	potassium channel tetramerisation domain containing 4	71063818	67516	NM_026214.3
Kctd5	potassium channel tetramerisation domain containing 5	1629	69259	NM_027008
Kctd6	potassium channel tetramerisation domain containing 6	74357550	71393	NM_027782.1
Kctd8	potassium channel tetramerisation domain containing 8	71670722	243043	NM_175519.3
Kctd9	potassium channel tetramerisation domain containing 9	70813924	105440	NM_134073.1
Kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	130912	68137	NM_133950.1
Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	2345	105785	NM_134090
Kdr	kinase insert domain protein receptor	2347	16542	NM_010612
Khdrbs3	KH domain containing, RNA binding, signal transduction associated 3	73769321	13992	NM_010158.1
Kif5a	kinesin family member 5A	2351	16572	NM_008447
Kif5b	kinesin family member 5B	2353	16573	NM_008448
Kif5c	kinesin family member 5C	74511818	16574	NM_008449.2
Kifc2	kinesin family member C2	614	16581	NM_010630
Kifc3	kinesin family member C3	71717081	16582	NM_010631.1
Kifc5a	kinesin family member C1	74658089	94116	NM_053173.1
Kirrel3	kin of IRRE like 3 (Drosophila)	71920516	67703	NM_026324.1
Kit	kit oncogene	73520994	16590	NM_021099.2
Kitl	kit ligand	616	17311	NM_013598
Kl	klotho	72119590	16591	NM_013823.1
Klc2	kinesin light chain 2	618	16594	NM_008451
Klf7	Kruppel-like factor 7 (ubiquitous)	2355	93691	NM_033563
Klhl1	kelch-like 1 (Drosophila)	73520995	93688	NM_053105.1
Klhl4	kelch-like 4 (Drosophila)	76115731	237010	NM_172781.1
Klhl9	kelch-like 9 (Drosophila)	74988762	242521	NM_172871.1
Klk10	kallikrein related-peptidase 10	70928269	69540	NM_133712.1
Knsl7	kinesin family member 15	1506		NM_010620
Kpna1	karyopherin (importin) alpha 1	2357	16646	NM_008465
Kpna4	karyopherin (importin) alpha 4	2359	16649	NM_008467
Kpnb1	karyopherin (importin) beta 1	77340472	16211	NM_008379.2
Kremen	kringle containing transmembrane protein 1	2362		NM_032396
Krt1-9	keratin 9	71670723	107656	NM_201255.1
Krtap12-1	keratin associated protein 12-1	1367	16694	NM_010670
L1cam	L1 cell adhesion molecule	620	16728	NM_008478
Laf4l	AF4/FMR2 family, member 4	2363		NM_033565
Lamb1-1	laminin B1 subunit 1	71670482	16777	NM_008482.1
Lamc1	laminin, gamma 1	623	226519	NM_010683
Lamc1	laminin, gamma 1	77868319	226519	NM_010683.1
Lamc2	laminin, gamma 2	74988766	16782	NM_008485.2
Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1	74881159	14768	NM_021295.1
Lancl3	LanC lantibiotic synthetase component C-like 3 (bacterial)	73925716	236285	NM_173414.1
Laptm4b	lysosomal-associated protein transmembrane 4B	75651225	114128	NM_033521.2

Large	like-glycosyltransferase	71670483	16795	NM_010687.1
Lass4	longevity assurance homolog 4 (S. cerevisiae)	176962	67260	NM_026058.2
Lat	linker for activation of T cells	2367	16797	NM_010689
Lats2	large tumor suppressor 2	73931411	50523	NM_015771.1
Lba1	lupus brain antigen 1	73907504	320429	XM_284542.3
Lcat	lecithin cholesterol acyltransferase	75042269	16816	NM_008490.1
Lct	lactase	73931621	226413	XM_129479.3
Ldb2	LIM domain binding 2	74641311	16826	NM_010698.2
Ldb3	LIM domain binding 3	2369	24131	NM_011918
Ldb3	LIM domain binding 3	77869087	24131	NM_011918.2
Ldhd	lactate dehydrogenase D	74425554	52815	NM_027570.3
Ldlr	low density lipoprotein receptor	1766	16835	NM_010700
Lef1	lymphoid enhancer binding factor 1	631	16842	NM_010703
Lef1	lymphoid enhancer binding factor 1	628	16842	NM_010703
Lef1	lymphoid enhancer binding factor 1	77866900	16842	NM_010703.2
Leng1	leukocyte receptor cluster (LRC) member 1	1641	69757	NM_027203
Leng5	leukocyte receptor cluster (LRC) member 1	1944	69757	NM_024168
Lepr	leptin receptor	73930822	16847	NM_010704.1
Lepre1	leprecan 1	2371	56401	NM_019782
Leprel2	leprecan-like 2	74047912	14789	NM_013534.3
Leprot	leptin receptor overlapping transcript	75773649	230514	NM_175036.2
Leprotl1	leptin receptor overlapping transcript-like 1	2373	68192	NM_026609
Lgals1	lectin, galactose binding, soluble 1	75651181	16852	NM_008495.1
Lgals1	lectin, galactose binding, soluble 1	70634417	16852	NM_008495.1
Lgi1	leucine-rich repeat LGI family, member 1	71670484	56839	NM_020278.2
Lgi2	leucine-rich repeat LGI family, member 2	71670485	246316	NM_144945.1
Lgi3	leucine-rich repeat LGI family, member 3	73520996	213469	NM_145219.2
Lgr5	leucine rich repeat containing G protein coupled receptor 5	72283791	14160	NM_010195.1
Lgr7	relaxin/insulin-like family peptide receptor 1	70562124	381489	NM_212452.1
Lgr8	relaxin/insulin-like family peptide receptor 2	73907500	140498	NM_080468.1
Lgtn	ligatin	323588	16865	NM_010709.1
Lhcgr	luteinizing hormone/choriogonadotropin receptor	72283794	16867	NM_013582.1
Lhcgr	luteinizing hormone/choriogonadotropin receptor	77869818	16867	NM_013582.1
Lhfp	lipoma HMGIC fusion partner	73769323	108927	NM_175386.3
Lhfp12	lipoma HMGIC fusion partner-like 2	72007934	218454	NM_172589.1
Lhfp13	lipoma HMGIC fusion partner-like 3	73635972	269629	XM_485569.1
Lhx1	LIM homeobox protein 1	633	16869	NM_008498
Lhx2	LIM homeobox protein 2	2375	16870	NM_010710
Lhx4	LIM homeobox protein 4	2377	16872	NM_010712
Lhx5	LIM homeobox protein 5	1369	16873	NM_008499
Lhx6	LIM homeobox protein 6	635	16874	NM_008500
Lhx8	LIM homeobox protein 8	2379	16875	NM_010713
Lhx9	LIM homeobox protein 9	2381	16876	NM_010714
Lifr	leukemia inhibitory factor receptor	71016573	16880	NM_013584.1
Lig1	ligase I, DNA, ATP-dependent	637	16881	NM_010715
Limk1	LIM-domain containing, protein kinase	640	16885	NM_010717
Limk2	LIM motif-containing protein kinase 2	61002	16886	NM_010718.1
Lims2	LIM and senescent cell antigen like domains 2	75145999	225341	NM_144862.1
Lin7a	lin-7 homolog A (C. elegans)	73520997	108030	XM_193582.4

Lip1	lysosomal acid lipase A	72129290	16889	NM_021460.1
Liph	lipase, member H	77280417	239759	NM_153404.1
Lip3	lipase, family member M	74272035	78753	XM_129247.5
Lix1	limb expression 1 homolog (chicken)	643	66643	NM_025681
Llg1h	lethal giant larvae homolog 1 (Drosophila)	645	16897	NM_008502
Lman1l	lectin, mannose-binding 1 like	70928340	235415	NM_146223.2
Lman2	lectin, mannose-binding 2	73718047	66890	NM_025828.2
Lmna	lamin A	73512494	16905	NM_001002011.1
Lmo1	LIM domain only 1	1373	109594	NM_057173
Lmo2	LIM domain only 2	2383	16909	NM_008505
Lmo3	LIM domain only 3	73616037	109593	NM_207222.1
Lmo4	LIM domain only 4	2385	16911	NM_010723
Lmod2	leiomodrin 2 (cardiac)	73636019	93677	XM_132983.3
Lmx1b	LIM homeobox transcription factor 1 beta	1508	16917	NM_010725
Lmyc1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	74881158	16918	NM_008506.2
Lnk	SH2B adaptor protein 3	1633	16923	NM_008507
LnX2	ligand of numb-protein X 2	75041516	140887	NM_080795.3
LOC114601	EH domain binding protein 1-like 1	73817932	114601	NM_053252.1
LOC213402	armadillo repeat containing 2	74988750	213402	XM_136978.3
LOC214238		74988751	214238	XM_134787.2
LOC217602	tetratricopeptide repeat domain 6	71670724	217602	XM_126988.3
LOC230251	zinc finger with KRAB and SCAN domains 16	74750043	230251	XM_143800.3
LOC230757	RIKEN cDNA 5730409E04Rik gene	74988752	230757	XM_131676.2
LOC233332	ADAM metalloproteinase with thrombospondin type 1 motif, 17	71924431	233332	XM_133542.3
LOC233637	-	73931418	233637	XM_133608.4
LOC235580		71924441	235580	XM_135159.3
LOC235953		73931419	235953	XM_135415.3
LOC238680	contactin associated protein-like 3	71924451	238680	XM_138666.3
LOC239556	calcium channel, voltage-dependent, alpha 1I subunit	74512007	239556	XM_139476.3
LOC241794	potassium voltage-gated channel, subfamily G, member 1	77340480	241794	XM_141545.3
LOC244958	-	71924480	244958	XM_147017.5
LOC245027	gene model 520, (NCBI)	74511966	245027	XM_147082.3
LOC270764		71924481	270764	XM_194744.3
LOC277860		74581425	277860	XM_203275.2
LOC329164	gene model 973, (NCBI)	74988753	381260	XM_286972.3
LOC329302		73931420	329302	XM_283676.3
LOC333605	FERM and PDZ domain containing 4	73931421	333605	XM_285569.3
LOC380720		73931422	380720	XM_358409.2
LOC380889	-	74988754	380889	XM_354799.2
LOC381076		72338724	381076	XM_354997.2
LOC381355	-	71924491	381355	XM_355321.2
LOC381557		71670744	381557	XM_355523.2
LOC381738	gene model 1060, (NCBI)	71670726	381738	XM_355721.2
LOC381742	trinucleotide repeat containing 18	74988756	381742	XM_355727.2
LOC381765	-	74425521	381765	XM_355761.2
LOC382102	gene model 1125, (NCBI)	71717570	382102	XM_356183.1
LOC382129		74047713	382129	XM_356226.2
LOC384349	gene model 1399, (NCBI)	71924184	384349	XM_357594.2
LOC384670	gene model 1441, (NCBI)	72109262	384670	XM_357782.2

LOC432420		71924492	432420	XM_488533.1
LOC432637	predicted gene, EG432637	74641294	432637	NM_001004167.1
LOC432641	-	73931423	432641	XM_488629.1
LOC432748		71924502	432748	XM_484244.1
LOC432855	zinc finger homeobox 2, antisense	74363340	432855	XM_488708.1
LOC432928		73931424	432928	XM_127956.1
LOC433022	phosphatidylinositol-specific phospholipase C, X domain containing 2	72008307	433022	XM_484546.1
LOC433088		71924504	433088	XM_488808.1
LOC433093		71924514	433093	XM_484621.1
LOC433228		73788454	433228	XM_488870.1
LOC433228		73788464	433228	XM_488870.1
LOC433254		72108822	433254	XM_484815.1
LOC433258		73931636	433258	XM_484817.1
LOC433311		74988757	433311	XM_488898.1
LOC433339		74988758	545352	XM_484902.1
LOC433402		73931425	433402	XM_484971.1
LOC433436		73636096	433436	XM_130312.4
LOC433485	predicted gene, OTTMUSG00000015750	73931426	433485	XM_485077.1
LOC433698	-	77340488	433698	XM_485371.1
LOC433708		72109295	433708	XM_485383.1
LOC433727		74363344	433727	XM_489051.1
LOC433740		77340490		XM_485420.1
LOC434002		74581371	434002	XM_489130.1
LOC434147	RIKEN cDNA D930028M14 gene	73512190	434147	XM_489169.1
LOC434236		73615572	434236	XM_485998.1
LOC434280	predicted gene, EG434280	72109337	434280	XM_486080.1
LOC434300		75988611	434300	XM_489233.1
LOC434368		74819253	434368	XM_486183.1
LOC434631		73512348	434631	XM_486487.1
LOC435626	RUN and FYVE domain containing 4	75041573	435626	XM_487601.1
LOC436099		73512350	436099	XM_488205.1
LOC544975		75144616	544975	XM_619153.1
Loh11cr2a	loss of heterozygosity, 11, chromosomal region 2, gene A homolog (human)	71836830	67776	NM_172767.2
Lonrf3	LON peptidase N-terminal domain and ring finger 3	75041538	74365	XM_135829.1
Loxl1	lysyl oxidase-like 1	70805934	16949	NM_010729.2
Loxl2	lysyl oxidase-like 2	71670486	94352	NM_033325.1
Lpd	acyl-CoA synthetase bubblegum family member 1	369		NM_053178
Lphn2	latrophilin 2	1768	99633	XM_131258
Lpin1	lipin 1	74819460	14245	NM_015763.2
Lpl	lipoprotein lipase	649	16956	NM_008509
Lrfrn2	leucine rich repeat and fibronectin type III domain containing 2	75041454	70530	XM_128642.1
Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	1371	16206	NM_008377
Lrmp	lymphoid-restricted membrane protein	74274684	16970	NM_008511.2
Lrp1b	low density lipoprotein-related protein 1B (deleted in tumors)	71670740	94217	NM_053011.1
Lrp4	low density lipoprotein receptor-related protein 4	71670487	228357	NM_172668.2
Lrp5	low density lipoprotein receptor-related protein 5	130331	16973	NM_008513.1
Lrp5	low density lipoprotein receptor-related protein 5	653	16973	NM_008513
Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	74047715	16975	NM_053073.1
Lrrc1	leucine rich repeat containing 1	74581426	214345	NM_172528.2

Lrrc16	leucine rich repeat containing 16	75042256	68732	NM_026825.1
Lrrc3	leucine rich repeat containing 3	1377	237387	NM_145152
Lrrc38	leucine rich repeat containing 38	72340184	242735	XM_144076.3
Lrrc3b	leucine rich repeat containing 3B	74881145	218763	NM_146052.2
Lrrc4	leucine rich repeat containing 4	75041463	192198	NM_138682.1
Lrrn1	leucine rich repeat protein 1, neuronal	72129293	16979	NM_008516.1
Lrrn2	leucine rich repeat protein 2, neuronal	74819328	16980	NM_010732.1
Lrrn3	leucine rich repeat protein 3, neuronal	75041464	16981	NM_010733.2
Lrrn6c	leucine rich repeat and Ig domain containing 2	72128919	242384	NM_175516.2
Lrrtm1	leucine rich repeat transmembrane neuronal 1	70805896	74342	NM_028880.2
Lrrtm3	leucine rich repeat transmembrane neuronal 3	73931637	216028	NM_178678.2
Lrsam1	leucine rich repeat and sterile alpha motif containing 1	74583161	227738	NM_199302.1
Lsamp	limbic system-associated membrane protein	625	268890	NM_175548
Lsp1	lymphocyte specific 1	2387	16985	NM_019391
Ltb	lymphotoxin B	74363350	16994	NM_008518.1
Ltbp3	latent transforming growth factor beta binding protein 3	76115733	16998	NM_008520.1
Ltbp4	latent transforming growth factor beta binding protein 4	76085748	108075	NM_175641.1
Ltk	leukocyte tyrosine kinase	75988666	17005	NM_008523.2
Lum	lumican	324012	17022	NM_008524.1
Lxn	latexin	72340108	17035	NM_016753.2
Ly6h	lymphocyte antigen 6 complex, locus H	71924388	23934	NM_011837.1
Lynx1	Ly6/neurotoxin 1	655	23936	NM_011838
Lypd1	Ly6/Plaur domain containing 1	72008305	72585	NM_145100.2
Lypd6	LY6/PLAUR domain containing 6	77332684		NM_177139.3
Lypla1	lysophospholipase 1	74047772	18777	NM_008866.2
Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2	74988572	70082	NM_027309.1
Lyst	lysosomal trafficking regulator	73994715	17101	NM_010748.1
Lzic	leucine zipper and CTNNBIP1 domain containing	276064	69151	NM_026963.2
Lzp-s	lysozyme	74819693	17110	NM_013590.2
Lztr1	leucine-zipper-like transcriptional regulator, 1	74047877	66863	NM_025808.2
Lzts1	leucine zipper, putative tumor suppressor 1	73994716	211134	NM_199364.1
Mad11l	mitotic arrest deficient 1-like 1	70928294	17120	NM_010752.1
Madcam1	mucosal vascular addressin cell adhesion molecule 1	2389	17123	NM_013591
Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	73771240	16658	NM_010658.2
Maged2	melanoma antigen, family D, 2	71836892	80884	NM_030700.1
Mageh1	melanoma antigen, family H, 1	17	75625	NM_023788
Magel2	melanoma antigen, family L, 2	71670488	27385	NM_013779.1
Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	73519705	14924	NM_010367.1
Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	75041515	99470	NM_133853.1
Magmas	mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction	2391	66449	NM_025571
Mal2	mal, T-cell differentiation protein 2	73994717	105853	NM_178920.2
Man1a	mannosidase 1, alpha	69120618	17155	NM_008548.2
Man2b1	mannosidase 2, alpha B1	75774113	17159	NM_010764.1
Manba	mannosidase, beta A, lysosomal	72007562	110173	NM_027288.2
Manea	mannosidase, endo-alpha	74882656	242362	NM_172865.2
Mansc1	MANSC domain containing 1	53	67729	NM_026345
Maoa	monoamine oxidase A	74750015	17161	NM_173740.1
Maob	monoamine oxidase B	71670489	109731	NM_172778.1
Map2k4	mitogen activated protein kinase kinase 4	276073	26398	NM_009157.2



Map2k5	mitogen activated protein kinase kinase 5	323585	23938	NM_011840.1
Map2k6	mitogen activated protein kinase kinase 6	73817433	26399	NM_011943.1
Map3k15	mitogen-activated protein kinase kinase kinase 15	73788442	270672	XM_486812.1
Map3k15	mitogen-activated protein kinase kinase kinase 15	73788441	270672	XM_486812.1
Map3k5	mitogen activated protein kinase kinase kinase 5	73994720	26408	NM_008580.1
Map3k7	mitogen activated protein kinase kinase kinase 7	2393	26409	NM_172688
Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	657	225028	XM_128800
Mapk11	mitogen-activated protein kinase 11	74357574	19094	NM_011161.4
Mapk12	mitogen-activated protein kinase 12	75988492	29857	NM_013871.2
Mapk12	mitogen-activated protein kinase 12	2395	29857	NM_013871
Mapk13	mitogen activated protein kinase 13	2397	26415	NM_011950
Mapk14	mitogen activated protein kinase 14	2399	26416	NM_011951
Mapk3	mitogen activated protein kinase 3	654927	26417	NM_011952.1
Mapk3	mitogen activated protein kinase 3	32576	26417	NM_011952.1
Mapk4	mitogen-activated protein kinase 4	73994721	225724	NM_172632.1
Mapk8	mitogen activated protein kinase 8	71063715	26419	NM_016700.2
Mapre1	microtubule-associated protein, RP/EB family, member 1	2401	13589	NM_007896
Mapre2	microtubule-associated protein, RP/EB family, member 2	659	212307	NM_153058
Mapt	microtubule-associated protein tau	67779684	17762	NM_010838.2
Mas1	MAS1 oncogene	73636100	17171	NM_008552.2
Mass1	G protein-coupled receptor 98	72081561	110789	XM_358310.2
Mast4	microtubule associated serine/threonine kinase family member 4	73929897	328329	XM_283179.3
Matk	megakaryocyte-associated tyrosine kinase	76135823	17179	NM_010768.1
Matn2	matrilin 2	73817421	17181	NM_016762.1
Matn4	matrilin 4	77371795	17183	NM_013592.2
Matr3	matrin 3	67752309	17184	NM_010771.3
Mbc2	membrane bound C2 domain containing protein	661	23943	NM_011843
Mbp	myelin basic protein	1225	17196	NM_010777
Mc3r	melanocortin 3 receptor	74511790	17201	NM_008561.2
Mc4r	melanocortin 4 receptor	663	17202	NM_016977
Mcam	melanoma cell adhesion molecule	71836841	84004	NM_023061.1
mCG1027775.1		73512351		
mCG1049722.1		74750076		
mCG10805.1		73512352		
mCG113702		73512353		
mCG114802.1		73512354		
mCG119642.1		74750263		
mCG140667		74641238		
mCG141917		75080643		
mCG142089		73512364		
mCG142691		73636029		
mCG145148		75080644		
mCG145698		73636030		
mCG145872		74512028		
mCG147095		73636031		
mCG147223		74641266		
mCG148338		75080645		
mCG148480		73512365		
mCG15583.2		75988632		

mCG5511.2		73636032	238321	
Mchr1	melanin-concentrating hormone receptor 1	74724669	207911	NM_145132.1
Mcl1	myeloid cell leukemia sequence 1	324009	17210	NM_008562.2
Mcm3ap	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	665	54387	NM_019434
Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	2403	17218	NM_008566
Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	71358638	17219	NM_008567.1
Mdfi	MyoD family inhibitor	321199	17240	NM_010783.1
Mdk	midkine	1227	17242	NM_010784
Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	74658090	107029	NM_145494.1
Mecp2	methyl CpG binding protein 2	2405	17257	NM_010788
Med8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	1595	80509	NM_020000
Mef2a	myocyte enhancer factor 2A	199392	17258	NM_013597.2
Mef2c	myocyte enhancer factor 2C	45665	17260	NM_025282.1
Mef2c	myocyte enhancer factor 2C	667	17260	NM_025282
Mef2d	myocyte enhancer factor 2D	67810540	17261	NM_133665.1
Meis1	myeloid ecotropic viral integration site 1	74047866	17268	NM_010789.1
Mela	melanoma antigen	74658083	17276	NM_008581.1
Mesdc2	mesoderm development candidate 2	72081556	67943	NM_023403.2
Mest	mesoderm specific transcript	71717082	17294	NM_008590.1
Met	met proto-oncogene	73787948	17295	NM_008591.1
Met	met proto-oncogene	73787949	17295	NM_008591.1
Mfap1	microfibrillar-associated protein 1A	74988551	67532	NM_026220.2
Mfap5	microfibrillar associated protein 5	67936206	50530	NM_015776.1
Mfn2	mitofusin 2	74882657	170731	NM_133201.1
Mfsd2	major facilitator superfamily domain containing 2	77280315	76574	XM_131683.3
Mgat2	mannoside acetylglucosaminyltransferase 2	74988614	217664	NM_146035.1
Mgat5	mannoside acetylglucosaminyltransferase 5	73931638	107895	NM_145128.2
MGC58970	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	70301277	237422	NM_183172.1
MGC59240	sphingosine-1-phosphate phosphatase 2	70301275	433323	NM_001004173.1
MGC67174	cDNA sequence BC057022	72077480	433940	NM_001004180.1
Mglap	matrix Gla protein	1229		NM_008597
Mgll	monoglyceride lipase	72129243	23945	NM_011844.3
Mgst3	microsomal glutathione S-transferase 3	71015350	66447	NM_025569.1
Midn	midnolin	71670739	59090	NM_021565.1
Mif	macrophage migration inhibitory factor	2407	17319	NM_010798
Mir16	membrane interacting protein of RGS16	356858	56209	NM_019580.3
Miz1	protein inhibitor of activated STAT 2	356088	17344	NM_008602.2
Mki67	antigen identified by monoclonal antibody Ki 67	1381	17345	XM_133912
Mlc1	megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human)	1770	170790	NM_133241
Mlp	MARCKS-like 1	670		NM_010807
Mlstd1	male sterility domain containing 1	71358652	330450	NM_178797.2
Mlx	MAX-like protein X	77414147	21428	NM_011550.2
Mm.119462		74750264		Mm.119462.0
Mm.25531		75041575		Mm.25531.0
Mm.26272		74640884		Mm.26272.0
Mm.271301		74641112		Mm.271301.0
Mm.341423		75988622		Mm.341423.0
Mm.376159		74641159		Mm.376159.0
Mm.86217		74641161		Mm.86217.0

Mm.96708		73615793		Mm.96708.0
Mmaa	methylmalonic aciduria (cobalamin deficiency) type A	1772	109136	NM_133823
Mme	membrane metallo endopeptidase	77371755	17380	NM_008604.2
Mme1	membrane metallo-endopeptidase-like 1	76135804	27390	NM_013783.1
Mmp14	matrix metallopeptidase 14 (membrane-inserted)	74658084	17387	NM_008608.2
Mmp15	matrix metallopeptidase 15	1383	17388	NM_008609
Mmp16	matrix metallopeptidase 16	72129244	17389	NM_019724.2
Mobk12b	MOB1, Mps One Binder kinase activator-like 2B (yeast)	70814343	214944	NM_178061.3
Mocs1	molybdenum cofactor synthesis 1	323590	56738	NM_020042.1
Mon1b	MON1 homolog b (yeast)	74958566	270096	NM_173015.1
Moxd1	monooxygenase, DBH-like 1	74357562	59012	NM_021509.3
Mpp3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	71920520	13384	NM_007863.1
Mpz1	myelin protein zero-like 1	77332711	68481	NM_001001880.1
Mras	muscle and microspikes RAS	72119592	17532	NM_008624.2
Mrc1	mannose receptor, C type 1	74581428	17533	NM_008625.1
Mrg1	myeloid ecotropic viral integration site-related gene 1	1231	17536	NM_010825
Mrg2	myeloid ecotropic viral integration site-related gene 2	74047845	17537	NM_008627.1
Mrpl12	mitochondrial ribosomal protein L12	70743841	56282	NM_027204.2
Mrpl39	mitochondrial ribosomal protein L39	673	27393	NM_017404
Mrpl54	mitochondrial ribosomal protein L54	74819464	66047	NM_025317.1
Mrps28	mitochondrial ribosomal protein S28	74425519	66230	NM_025434.2
Mrps28	mitochondrial ribosomal protein S28	75259441	66230	NM_025434.2
Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B	293474	69774	NM_027209.2
Msh2	mutS homolog 2 (E. coli)	74657951	17685	NM_008628.1
Msi2h	Musashi homolog 2 (Drosophila)	73616034	76626	NM_054043.1
Msn	moesin	74658085	17698	NM_010833.1
Msr2	macrophage scavenger receptor 2	1896	80891	NM_030707
Msrb	methionine sulfoxide reductase B2	1774		NM_029619
Msrb2	methionine sulfoxide reductase B2	76135795	76467	NM_029619.2
Mt3	metallothionein 3	75079775	17751	NM_013603.1
Mtap1a	microtubule-associated protein 1 A	76115734	17754	XM_194040.4
Mtap2	microtubule-associated protein 2	74272037	17756	NM_008632.1
Mtap4	microtubule-associated protein 4	71587919	17758	NM_008633.1
Mtch2	mitochondrial carrier homolog 2 (C. elegans)	72080084	56428	NM_019758.2
Mtf1	metal response element binding transcription factor 1	2409	17764	NM_008636
Mtf2	metal response element binding transcription factor 2	1510	17765	NM_013827
Mtif2	mitochondrial translational initiation factor 2	677	76784	NM_133767
Mtmr6	myotubularin related protein 6	74658087	219135	NM_144843.2
Mtmr7	myotubularin related protein 7	45669	54384	NM_019433.1
mt-Nd3		675		NC_001569
Mtpn	myotrophin	2411	14489	NM_008098
Mtrr	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	2413	210009	NM_172480
Mtss1	metastasis suppressor 1	1776	211401	NM_144800
Mtvr2	mammary tumor virus receptor 2	1898	17826	NM_023166
Mum111	melanoma associated antigen (mutated) 1-like 1	74357565	245631	NM_175541.2
Mup2	major urinary protein 2	680	17841	NM_008647
Mup5	major urinary protein 5	73997144	17844	NM_008649.1
Mvp	major vault protein	321202	78388	NM_080638.1
Mx1	myxovirus (influenza virus) resistance 1	1385	17857	NM_010846

Mx2	myxovirus (influenza virus) resistance 2	1778	17858	NM_013606
Mxd4	Max dimerization protein 4	67810541	17122	NM_010753.2
Mxi1	Max interacting protein 1	74819343	17859	NM_010847.1
Myadm	myeloid-associated differentiation marker	74658086	50918	NM_016969.1
Myb	myeloblastosis oncogene	1512	17863	NM_010848
Myc	myelocytomatosis oncogene	2415	17869	NM_010849
Myl4	myosin, light polypeptide 4	72129251	17896	NM_010858.3
Myliip	myosin regulatory light chain interacting protein	77278965	218203	NM_153789.2
Myik	myosin, light polypeptide kinase	74819252	107589	NM_139300.2
Myo10	myosin X	74743255	17909	NM_019472.1
Myo1b	myosin IB	72080133	17912	NM_010863.1
Myo5b	myosin Vb	73592538	17919	NM_201600.1
Myo5c	myosin VC	75042249	208943	XM_198225.4
Myst1	MYST histone acetyltransferase 1	2417	67773	NM_026370
Myt1	myelin transcription factor 1	71924077	17932	NM_008665.2
Nab1	Ngfi-A binding protein 1	70743878	17936	NM_008667.2
Nap1l5	nucleosome assembly protein 1-like 5	72080123	58243	NM_021432.1
Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	75651234	17957	NM_019632.1
Nat6	N-acetyltransferase 6	1780	56441	NM_019750
Nav1	neuron navigator 1	77371765	215690	NM_173437.1
Nbr1	neighbor of Brca1 gene 1	1235	17966	NM_008676
Ncald	neurocalcin delta	71924321	52589	NM_134094.2
Ncam2	neural cell adhesion molecule 2	682	17968	NM_010954
Ncdn	neurochondrin	684	26562	NM_011986
Ncoa4	nuclear receptor coactivator 4	1782	27057	NM_019744
Ncoa7	nuclear receptor coactivator 7	77340496	211329	NM_172495.2
Ncor1	nuclear receptor co-repressor 1	686	20185	NM_011308
Nde1	nuclear distribution gene E homolog 1 (A nidulans)	67779875	67203	NM_023317.1
Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	1514	83431	NM_023668
Ndn	necdin	688	17984	NM_010882
Ndr2	N-myc downstream regulated gene 2	1237	29811	NM_013864
Ndr3	N-myc downstream regulated gene 3	690	29812	NM_013865
Ndst3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	75041473	83398	NM_031186.1
Ndst4	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	74511837	64580	NM_022565.1
Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	74658173	67273	NM_024197.1
Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	74743256	67264	NM_026061.1
Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	2421	227197	NM_145518
Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	74818622	226646	NM_153064.3
Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	74819243	225887	NM_144870.2
Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	77371763	72900	XM_128725.4
Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	74047904	83814	NM_031881.1
Nef3	neurofilament, medium polypeptide	73817434	18040	NM_008691.1
Nefh	neurofilament, heavy polypeptide	74512048	380684	NM_010904.2
Negr1	neuronal growth regulator 1	692	320840	NM_177274
Neil3	nei like 3 (E. coli)	74658247	234258	NM_146208.1
Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	75042263	18005	NM_010892.1
Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	72339542	59125	NM_021605.2
Nell2	NEL-like 2 (chicken)	72103854	54003	NM_016743.1
Nenf	neuron derived neurotrophic factor	74272919	66208	NM_025424.1

Nes	nestin	1387	18008	NM_016701
Net1	neuroepithelial cell transforming gene 1	74581396	56349	NM_019671.1
Neto1	neuropilin (NRP) and tolloid (TLL)-like 1	72129248	246317	NM_144946.2
Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	75084453	74513	XM_134498.5
Neu2	neuraminidase 2	75084472	23956	NM_015750.1
Neurl	neuralized-like homolog (Drosophila)	73769327	18011	NM_021360.2
Neurod1	neurogenic differentiation 1	75650865	18012	NM_010894.1
Neurod1	neurogenic differentiation 1	696	18012	NM_010894
Neurod2	neurogenic differentiation 2	75651126	18013	NM_010895.2
Neurod2	neurogenic differentiation 2	74750018	18013	NM_010895.2
Neurod6	neurogenic differentiation 6	698	11922	NM_009717
Nfia	nuclear factor I/A	1239	18027	NM_010905
Nfib	nuclear factor I/B	1555	18028	NM_008687
Nfic	nuclear factor I/C	74988734	18029	NM_008688.2
Nfil3	nuclear factor, interleukin 3, regulated	70743904	18030	NM_017373.2
Nfix	nuclear factor I/X	2423	18032	NM_010906
Nfix	nuclear factor I/X	77413698	18032	NM_010906.1
Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	2425	18037	NM_008690
Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	67870467	18041	NM_010911.1
Nfxl1	nuclear transcription factor, X-box binding-like 1	76135740	100978	XM_358354.1
Nfyc	nuclear transcription factor-Y gamma	1900	18046	NM_008692
Ngb	neuroglobin	2427	64242	NM_022414
Ngef	neuronal guanine nucleotide exchange factor	72119591	53972	NM_019867.1
Ngef	neuronal guanine nucleotide exchange factor	72129292	53972	NM_019867.1
Ngfb	nerve growth factor, beta	74581384	18049	NM_013609.1
Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	705	18053	NM_033217
Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	1784	18053	NM_033217
Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1	1786	12070	NM_009750
Ngp	neutrophilic granule protein	73997145	18054	NM_008694.1
Nhlh1	nescient helix loop helix 1	75077191	18071	NM_010916.1
Nhlh2	nescient helix loop helix 2	74657929	18072	NM_178777.2
Nhlrc1	NHL repeat containing 1	75084473	105193	NM_175340.2
Niban	niban protein	73931639	63913	NM_022018.1
Nicn1	nicotin 1	75773512	66257	NM_025449.2
Nid1	nidogen 1	75084474	18073	NM_010917.1
Nifun	IscU iron-sulfur cluster scaffold homolog (E. coli)	74819565	66383	NM_025526.1
Nin	ninein	76115736	18080	NM_008697.1
Ninj1	ninjurin 1	71670490	18081	NM_013610.1
Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	75041549	93790	NM_023647.2
Nkd1	naked cuticle 1 homolog (Drosophila)	74586666	93960	NM_027280.2
Nkd2	naked cuticle 2 homolog (Drosophila)	75042259	72293	NM_028186.2
Nkiras2	NFkB inhibitor interacting Ras-like protein 2	2429	71966	NM_028024
Nlk	nemo like kinase	76085742	18099	NM_008702.2
Nmb	neuromedin B	71836874	68039	NM_026523.1
Nmbr	neuromedin B receptor	77332086	18101	NM_008703.1
Nme1	expressed in non-metastatic cells 1, protein	75144617	18102	NM_008704.2
Nnat	neuronatin	655497	18111	NM_010923.1
Nnat	neuronatin	77887874	18111	NM_010923.1
Nnp1	ribosomal RNA processing 1 homolog (S. cerevisiae)	713	18114	NM_010925

Nog	noggin	75084476	18121	NM_008711.1
Nol4	nucleolar protein 4	76115737	319211	NM_199024.1
Nola3	nucleolar protein family A, member 3	75042268	66181	NM_025403.1
Nos1	nitric oxide synthase 1, neuronal	75147762	18125	NM_008712.1
Nos1ap	nitric oxide synthase 1 (neuronal) adaptor protein	77280574	70729	XM_129577.4
Notch3	Notch gene homolog 3 (Drosophila)	1788	18131	NM_008716
Nov	nephroblastoma overexpressed gene	69120620	18133	NM_010930.3
Nov	nephroblastoma overexpressed gene	1241	18133	NM_010930
Nova1	neuro-oncological ventral antigen 1	73931640	18134	XM_356586.2
Npas2	neuronal PAS domain protein 2	74724764	18143	NM_008719.1
Npc2	Niemann Pick type C2	75774115	67963	NM_023409.3
Npdc1	neural proliferation, differentiation and control gene 1	715	18146	NM_008721
Npepps	aminopeptidase puromycin sensitive	844	19155	NM_008942
Npnt	nephronectin	71670677	114249	NM_033525.1
Npr1	natriuretic peptide receptor 1	71670678	18160	NM_008727.4
Npr3	natriuretic peptide receptor 3	73931412	18162	NM_008728.1
Nptx1	neuronal pentraxin 1	73520998	18164	NM_008730.1
Nptx2	neuronal pentraxin 2	74047773	53324	NM_016789.2
Npy	neuropeptide Y	717	109648	NM_023456
Npy1r	neuropeptide Y receptor Y1	72103807	18166	NM_010934.1
Nqo1	NAD(P)H dehydrogenase, quinone 1	74800915	18104	NM_008706.1
Nqo2	NAD(P)H dehydrogenase, quinone 2	74819244	18105	NM_020282.2
Nqo3a2	cytochrome b5 reductase 1	74988452	72017	NM_028057.1
Nr1d1	nuclear receptor subfamily 1, group D, member 1	1243	217166	NM_145434
Nr1d2	nuclear receptor subfamily 1, group D, member 2	1245	353187	NM_011584
Nr1h3	nuclear receptor subfamily 1, group H, member 3	2431	22259	NM_013839
Nr2e3	nuclear receptor subfamily 2, group E, member 3	2434	23958	NM_013708
Nr2e3	nuclear receptor subfamily 2, group E, member 3	2433	23958	NM_013708
Nr2f1	nuclear receptor subfamily 2, group F, member 1	720	13865	NM_010151
Nr2f2	nuclear receptor subfamily 2, group F, member 2	725	11819	NM_009697
Nr2f6	nuclear receptor subfamily 2, group F, member 6	2436	13864	NM_010150
Nr3c1	nuclear receptor subfamily 3, group C, member 1	727	14815	NM_008173
Nr3c2	nuclear receptor subfamily 3, group C, member 2	730	110784	XM_356093
Nr4a1	nuclear receptor subfamily 4, group A, member 1	1792	15370	NM_010444
Nr4a2	nuclear receptor subfamily 4, group A, member 2	732	18227	NM_013613
Nr5a1	nuclear receptor subfamily 5, group A, member 1	734	26423	NM_139051
Nrbf2	nuclear receptor binding factor 2	1902	641340	NM_025307
Nrbp2	nuclear receptor binding protein 2	75774686	223649	NM_144847.1
Nrf1	nuclear respiratory factor 1	2438	50777	NM_010938
Nrg1	neuregulin 1	74743257	211323	XM_486093.1
Nrgn	neurogranin	69153759	64011	NM_022029.1
Nrgn	neurogranin	736	18181	NM_022029
Nrip1	nuclear receptor interacting protein 1	739	64011	NM_173440
Nrip3	nuclear receptor interacting protein 3	73520999	78593	NM_020610.1
Nrk	Nik related kinase	75084477	27206	NM_013724.1
Nrm	nurim (nuclear envelope membrane protein)	75042265	106582	NM_134122.1
Nrn1	neuritin 1	75147760	68404	NM_153529.1
Nrp1	neuropilin 1	74272479	18186	NM_008737.1
Nrsn2	neurensin 2	77280555	268903	XM_130718.6

Nrtn	neurturin	741	18188	NM_008738
Nrxn1	neurexin I	70301083	18189	NM_020252.1
Nrxn3	neurexin III	71587783	18191	NM_172544.1
Nsdhl	NAD(P) dependent steroid dehydrogenase-like	72007933	18194	NM_010941.3
Nsep1	Y box protein 1	743		NM_011732
Nsf	N-ethylmaleimide sensitive fusion protein	356092	18195	NM_008740.2
Nsun7	NOL1/NOP2/Sun domain family, member 7	77332090		NM_027602.1
Nt5m	5',3'-nucleotidase, mitochondrial	74658088	103850	NM_134029.1
Ntf3	neurotrophin 3	2440	18205	NM_008742
Ntf5	neurotrophin 5	1393	78405	NM_198190
Ntn1	netrin 1	74511838	18208	NM_008744.1
Ntng1	netrin G1	71924185	80883	NM_030699.1
Ntng2	netrin G2	73615803	171171	NM_133500.1
Ntrk1	neurotrophic tyrosine kinase, receptor, type 1	71670679	18211	XM_283871.1
Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	746	18212	NM_008745
Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	76115738	18213	NM_008746.4
Nts	neurotensin	73788032	67405	NM_024435.2
Ntsr1	neurotensin receptor 1	73519704	18216	NM_018766.1
Nubp1	nucleotide binding protein 1	74819687	26425	NM_011955.1
Nucb2	nucleobindin 2	75774683	53322	NM_016773.1
Nudc	nuclear distribution gene C homolog (Aspergillus)	2442	18221	NM_010948
Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	275870	66401	NM_025539.1
Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	77414917	66401	NM_025539.1
Nudt4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	71836882	71207	NM_027722.2
Nudt9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	2444	74167	NM_028794
Numa1	nuclear mitotic apparatus protein 1	74988615	101706	NM_133947.2
Nup93	nucleoporin 93	75774679	71805	NM_172410.1
Nvl	nuclear VCP-like	5	67459	NM_026171
Nxf1	nuclear RNA export factor 1 homolog (S. cerevisiae)	356089	53319	NM_016813.2
Nxf7	nuclear RNA export factor 7	75988557	170722	NM_130888.1
Nxn	nucleoredoxin	72007747	18230	NM_008750.2
Nxph1	neurexophilin 1	75084479	18231	NM_008751.2
Nxph3	neurexophilin 3	356852	104079	NM_130858.1
Nxph4	neurexophilin 4	73521000	104080	NM_183297.1
Oaz2	ornithine decarboxylase antizyme 2	748	18247	NM_010952
Obfc1	oligonucleotide/oligosaccharide-binding fold containing 1	1938	108689	NM_175360
Ociad2	OCIA domain containing 2	75041527	433904	XM_485628.1
Odc1	ornithine decarboxylase, structural 1	74583117	18263	NM_013614.1
Odz2	odd Oz/ten-m homolog 2 (Drosophila)	72008308	23964	NM_011856.2
Odz3	odd Oz/ten-m homolog 3 (Drosophila)	752	23965	NM_011857
Odz4	odd Oz/ten-m homolog 4 (Drosophila)	754	23966	NM_011858
Og9x	SEBOX homeobox	756	18292	NM_008759
Ogfr	opioid growth factor receptor	67809268	72075	NM_031373.2
Ogfrl1	opioid growth factor receptor-like 1	73818756	70155	XM_129809.6
Ogn	osteoglycin	2446	18295	NM_008760
Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl tra	758	108155	NM_139144
Oit1	oncoprotein induced transcript 1	227164	18300	NM_146050.1
Olfm1	olfactomedin 1	760	56177	NM_019498
Olfm2	olfactomedin 2	71717155	244723	NM_173777.2

Olfml3	olfactomedin-like 3	77280333	99543	NM_133859.1
Olig2	oligodendrocyte transcription factor 2	2448	50913	NM_016967
Omg	oligodendrocyte myelin glycoprotein	2450	18377	NM_019409
Opcml	opioid binding protein/cell adhesion molecule-like	73992920	330908	NM_177906.3
Opn1sw	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)	75773699	12057	NM_007538.2
Opn3	opsin (encephalopsin)	71020433	13603	NM_010098.1
Oprl1	opioid receptor-like 1	75077232	18389	NM_011012.2
Oprs1	opioid receptor, sigma 1	1794	18391	NM_011014
Optn	optineurin	2452	71648	NM_181848
ORF19	open reading frame 19	1796	68767	XM_128709
ORF21	SET domain containing 4	1798		NM_145482
ORF34	open reading frame 34	74581430	207375	NM_198105.1
ORF5	RWD domain containing 2B	1587	53858	NM_016924
ORF63	open reading frame 63	1247	224419	NM_144854
Osbpl10	oxysterol binding protein-like 10	71015387	74486	NM_148958.1
Osbpl3	oxysterol binding protein-like 3	70231995	71720	NM_027881.1
Osbpl5	oxysterol binding protein-like 5	73997146	79196	NM_024289.1
Osbpl6	oxysterol binding protein-like 6	70744325	99031	NM_145525.1
Osbpl8	oxysterol binding protein-like 8	74641162	237542	NM_001003717.1
Osbpl9	oxysterol binding protein-like 9	77371759	100273	NM_133885.1
Ostf1	osteoclast stimulating factor 1	73907505	20409	NM_017375.1
Ostn	osteocrin	74581440	239790	NM_198112.1
Otc	ornithine transcarbamylase	74581369	18416	NM_008769.2
Otof	otoferlin	73788043	83762	NM_031875.1
Otof	otoferlin	73788044	83762	NM_031875.1
Otp	orthopedia homolog (Drosophila)	2454	18420	NM_011021
Otx1	orthodenticle homolog 1 (Drosophila)	762	18423	NM_011023
Otx3	diencephalon/mesencephalon homeobox 1	1484		NM_130865
Ovgp1	oviductal glycoprotein 1	71670680	12659	NM_007696.2
Oxct1	3-oxoacid CoA transferase 1	655499	67041	NM_024188.3
Oxct1	3-oxoacid CoA transferase 1	77869796	67041	NM_024188.3
Oxr1	oxidation resistance 1	72129295	170719	NM_130885.1
Oxtr	oxytocin receptor	75081001	18430	XM_144956.3
P2rx1	purinergic receptor P2X, ligand-gated ion channel, 1	75890835	18436	NM_008771.2
P2rx2	purinergic receptor P2X, ligand-gated ion channel, 2	75551473	231602	NM_153400.2
P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3	75888751	228139	NM_145526.1
P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	75551474	18438	NM_011026.1
P2rx5	purinergic receptor P2X, ligand-gated ion channel, 5	75551475	94045	NM_033321.1
P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	75551477	18439	NM_011027.1
P2rxl1	purinergic receptor P2X-like 1, orphan receptor	75551463	18440	NM_011028.1
P2ry12	purinergic receptor P2Y, G-protein coupled 12	1906	70839	NM_027571
P2ry14	purinergic receptor P2Y, G-protein coupled, 14	76135748	140795	NM_133200.2
P2ry14	purinergic receptor P2Y, G-protein coupled, 14	2269	140795	NM_133200
P2ry2	purinergic receptor P2Y, G-protein coupled 2	75144693	18442	NM_008773.2
P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6	1800	233571	NM_183168
P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	73732152	18452	NM_011031.1
P4hb	prolyl 4-hydroxylase, beta polypeptide	74658245	18453	NM_011032.1
P518	pyroglutamylated RFamide peptide	75041585	227717	NM_183424.1
Pacrg	Park2 co-regulated	74743258	69310	XM_128418.2



Pacs1l	phosphofurin acidic cluster sorting protein 2	73635816	217893	XM_203601.4
Pacsin1	protein kinase C and casein kinase substrate in neurons 1	74047926	23969	NM_011861.1
Pacsin2	protein kinase C and casein kinase substrate in neurons 2	74047920	23970	NM_011862.1
Paf1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	293469	54624	NM_019458.2
Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	2460	18472	NM_013625
Paip2	polyadenylate-binding protein-interacting protein 2	357095	67869	NM_026420.1
Paip2	polyadenylate-binding protein-interacting protein 2	77869857	67869	NM_026420.1
Pak1	p21 (CDKN1A)-activated kinase 1	73521001	18479	NM_011035.1
Pak3	p21 (CDKN1A)-activated kinase 3	71836887	18481	NM_008778.1
Pak6	p21 (CDKN1A)-activated kinase 6	75084501	214230	XM_111790.5
Pak7	p21 (CDKN1A)-activated kinase 7	75988567	241656	NM_172858.1
Pald	cDNA sequence X99384	71670681	27355	NM_013753.1
Palm2	paralemmin 2	74581441	242481	NM_172868.1
Palmd	palmdelphin	74581442	114301	NM_023245.2
Pam	peptidylglycine alpha-amidating monooxygenase	73997147	18484	NM_013626.1
Panx2	pannexin 2	74581443	406218	NM_001002005.1
Papola	poly (A) polymerase alpha	1251	18789	NM_011112
Pappa	pregnancy-associated plasma protein A	74581444	18491	XM_131437.5
Pappa2	pappalysin 2	276066	23850	XM_355248.2
Paqr4	progesterone and adipoQ receptor family member IV	248335	76498	NM_023824.2
Paqr8	progesterone and adipoQ receptor family member VIII	74724530	74229	NM_028829.3
Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	73992915	93742	NM_033620.1
Park2	parkin	2462	50873	NM_016694
Parp8	poly (ADP-ribose) polymerase family, member 8	74819242	52552	NM_027272.3
Parva	parvin, alpha	75077213	57342	NM_020606.4
Parvb	parvin, beta	77332713	170736	NM_133167.2
Parvg	parvin, gamma	70813925	64099	NM_022321.2
Pax3	paired box gene 3	2464	18505	NM_008781
Pax6	paired box gene 6	72007748	18508	NM_013627.2
Pax6	paired box gene 6	764	18508	NM_013627
Pax7	paired box gene 7	766	18509	NM_011039
Pax9	paired box gene 9	2466	18511	NM_011041
Pbx3	pre B-cell leukemia transcription factor 3	76085744	18516	NM_016768.1
Pcbd	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	1802		NM_025273
Pcbp3	poly(rC) binding protein 3	768	59093	NM_021568
Pcbp4	poly(rC) binding protein 4	67936208	59092	NM_021567.2
Pcdh1	protocadherin 1	75934527	75599	NM_029357.2
Pcdh11x	protocadherin 11 X-linked	73521002	245578	XM_142105.3
Pcdh18	protocadherin 18	71358554	73173	NM_130448.2
Pcdh20	protocadherin 20	71670738	219257	NM_178685.3
Pcdh21	protocadherin 21	72104186	170677	NM_130878.2
Pcdh7	protocadherin 7	73521003	54216	NM_018764.1
Pcdh8	protocadherin 8	74750019	18530	NM_021543.1
Pcdh9	protocadherin 9	10	211712	XM_139187
Pcdha10	protocadherin alpha 10	1253	12943	NM_009961
Pcdhac1	protocadherin alpha subfamily C, 1	73512189	353236	NM_001003671.1
Pcdhb13	protocadherin beta 13	74743259	93884	NM_053138.1
Pcdhb16	protocadherin beta 16	72340179	93887	NM_053141.2
Pcdhb17	protocadherin beta 17	1908	93888	NM_053142

Pcdhb18	protocadherin beta 18	74581445	93889	NM_053143.1
Pcdhb19	protocadherin beta 19	74743270	93890	NM_053144.1
Pcdhb2	protocadherin beta 2	74743271	93873	NM_053127.1
Pcdhb20	protocadherin beta 20	2468	93891	NM_053145
Pcdhb9	protocadherin beta 9	73512187	93880	NM_053134.2
Pcdhga12	protocadherin gamma subfamily A, 12	770	93724	NM_033595
Pcdhga5	protocadherin gamma subfamily A, 5	72338695	93713	NM_033588.2
Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	71836804	74551	NM_028994.1
Pclo	piccolo (presynaptic cytomatrix protein)	71670682	26875	NM_011995.2
Pcnt2	pericentrin (kendrin)	1255		NM_008787
Pcp2	Purkinje cell protein 2 (L7)	655115	18545	NM_008790.1
Pcp2	Purkinje cell protein 2 (L7)	77413702	18545	NM_008790.1
Pcp4	Purkinje cell protein 4	772	18546	NM_008791
Pcp4l1	Purkinje cell protein 4-like 1	75084520	66425	XM_484933.1
Pcsk1	proprotein convertase subtilisin/kexin type 1	72008494	18548	NM_013628.1
Pcsk1	proprotein convertase subtilisin/kexin type 1	2470	18548	NM_013628
Pcsk1n	proprotein convertase subtilisin/kexin type 1 inhibitor	777	30052	NM_013892
Pcsk2	proprotein convertase subtilisin/kexin type 2	72080025	18549	NM_008792.3
Pcsk5	proprotein convertase subtilisin/kexin type 5	70616019	18552	XM_129214.3
Pcsk6	proprotein convertase subtilisin/kexin type 6	75084491	18553	XM_355911.2
Pcyt1b	phosphate cytidyltransferase 1, choline, beta isoform	74641319	236899	NM_177546.2
Pdcd4	programmed cell death 4	73931413	18569	NM_011050.1
Pdcl	phosducin-like	324213	67466	NM_026176.2
Pde10a	phosphodiesterase 10A	71924204	23984	NM_011866.1
Pde11a	phosphodiesterase 11A	75081007	241489	XM_140993.4
Pde1a	phosphodiesterase 1A, calmodulin-dependent	782	18573	NM_016744
Pde1b	phosphodiesterase 1B, Ca2+-calmodulin dependent	1257	18574	NM_008800
Pde1c	phosphodiesterase 1C	1804	18575	NM_011054
Pde3a	phosphodiesterase 3A, cGMP inhibited	71717083	54611	NM_018779.1
Pde4a	phosphodiesterase 4A, cAMP specific	1806	18577	NM_019798
Pde4b	phosphodiesterase 4B, cAMP specific	2472	18578	NM_019840
Pde4d	phosphodiesterase 4D, cAMP specific	1259	238871	NM_011056
Pde5a	phosphodiesterase 5A, cGMP-specific	73931641	242202	NM_153422.1
Pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamma	72104173	18588	NM_012065.2
Pde7b	phosphodiesterase 7B	71670683	29863	NM_013875.2
Pde8b	phosphodiesterase 8B	71020389	218461	NM_172263.1
Pde9a	phosphodiesterase 9A	785	18585	NM_008804
Pdgfa	platelet derived growth factor, alpha	1516	18590	NM_008808
Pdgfb	platelet derived growth factor, B polypeptide	71587782	18591	NM_011057.2
Pdgfd	platelet-derived growth factor, D polypeptide	1910	71785	NM_027924
Pdgfra	platelet derived growth factor receptor, alpha polypeptide	77280309	18595	NM_011058.1
Pdgfrb	platelet derived growth factor receptor, beta polypeptide	77278981	18596	NM_008809.1
Pdha1	pyruvate dehydrogenase E1 alpha 1	323397	18597	NM_008810.2
Pdia5	protein disulfide isomerase associated 5	75042262	72599	NM_028295.1
Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3	2474	236900	NM_145630
Pdlim2	PDZ and LIM domain 2	2476	213019	NM_145978
Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	788	216134	NM_172134
Pdyn	prodynorphin	71717084	18610	NM_018863.2
Pdzk3	PDZ domain containing 2	74988286	68070	XM_127972.3

Pdzk8	PDZ domain containing 8	74047716	107368	XM_140761.5
Pdzrn3	PDZ domain containing RING finger 3	71836787	55983	NM_018884.1
Pdzx	MAGI family member, X-linked	74581446	54634	NM_018832.1
Pea15	phosphoprotein enriched in astrocytes 15A	70928292	18611	NM_008556.1
Pea15	phosphoprotein enriched in astrocytes 15A	77414654	18611	NM_008556.1
Peg10	paternally expressed 10	74357549	170676	NM_130877.1
Pelo	pelota homolog (Drosophila)	789	105083	NM_134058
Penk1	preproenkephalin 1	74881286	18619	NM_001002927.1
Per1	period homolog 1 (Drosophila)	791	18626	NM_011065
Per2	period homolog 2 (Drosophila)	793	18627	NM_011066
Per3	period homolog 3 (Drosophila)	75084530	18628	NM_011067.1
Pex13	peroxisomal biogenesis factor 13	74658240	72129	NM_023651.2
Pex14	peroxisomal biogenesis factor 14	1397	56273	NM_019781
Pex2	peroxin 2	74581447	58869	NM_021483.1
Pfdn4	prefoldin 4	74882686	109054	XM_355370.2
Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	1399	18640	NM_008825
Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	74657950	170768	NM_133232.1
Pfkl	phosphofructokinase, liver, B-type	795	18641	NM_008826
Pfkm	phosphofructokinase, muscle	67870466	18642	NM_021514.2
Pfkp	phosphofructokinase, platelet	61412	56421	NM_019703.2
Pfn2	profilin 2	1261	18645	NM_019410
Pftk1	PFTAIRe protein kinase 1	71670684	18647	NM_011074.1
Pgbd5	piggyBac transposable element derived 5	73931642	209966	NM_171824.1
Pgf	placental growth factor	121099	18654	NM_008827.2
Pgf	placental growth factor	77869838	18654	NM_008827.2
Pgm2l1	phosphoglucomutase 2-like 1	70615597	70974	NM_027629.1
Pgr15l	G protein-coupled receptor 15-like	73615804	245526	XM_142008.3
Pgrmc1	progesterone receptor membrane component 1	797	53328	NM_016783
Pgrmc1	progesterone receptor membrane component 1	2478	53328	NM_016783
Pgrmc2	progesterone receptor membrane component 2	74882697	70804	XM_130859.5
Phactr1	phosphatase and actin regulator 1	71920511	218194	XM_356658.2
Phactr2	phosphatase and actin regulator 2	73521004	215789	XM_125520.5
Phactr4	phosphatase and actin regulator 4	71924214	100169	NM_175306.2
Phf1	PHD finger protein 1	356287	21652	NM_009343.1
Phf6	PHD finger protein 6	72080044	70998	NM_027642.1
Phldb2	pleckstrin homology-like domain, family B, member 2	74512017	208177	NM_153412.1
Phospho1	phosphatase, orphan 1	71670685	237928	NM_153104.1
Phox2b	paired-like homeobox 2b	2480	18935	NM_008888
Phyh	phytanoyl-CoA hydroxylase	74800914	16922	NM_010726.1
Phyhip	phytanoyl-CoA hydroxylase interacting protein	544328	105653	NM_145981.1
Phyhipl	phytanoyl-CoA hydroxylase interacting protein-like	544326	70911	NM_178621.2
Pi4k2a	phosphatidylinositol 4-kinase type 2 alpha	74047913	84095	NM_145501.1
Pias4	protein inhibitor of activated STAT 4	323587	59004	NM_021501.1
Pias4	protein inhibitor of activated STAT 4	77414895	59004	NM_021501.1
Pib5pa	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	71670686	170835	NM_172439.1
Pib5pa	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	77869865	170835	NM_172439.1
Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	356489	14755	NM_011822.2
Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	1810	78928	NM_133779
Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	74583163	18710	NM_181585.4

Pim2	proviral integration site 2	32583	18715	NM_138606.1
Pip3ap	myotubularin related protein 12	70431435	268783	NM_172958.2
Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	74425520	18719	NM_008846.1
Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	77887888	18719	NM_008846.1
Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma	71836809	18717	NM_008844.1
Pip5k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	75146004	18718	NM_008845.2
Pip5k2c	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	799	117150	NM_054097
Pir	pirin	67870113	69656	NM_027153.1
Pir	pirin	75651229	69656	NM_027153.1
Pitpnm2	phosphatidylinositol transfer protein, membrane-associated 2	73997148	19679	NM_011256.1
Pitrm1	pitrilysin metallopeptidase 1	74273117	69617	NM_145131.1
Pitx1	paired-like homeodomain transcription factor 1	199398	18740	NM_011097.1
Pitx2	paired-like homeodomain transcription factor 2	802	18741	NM_011098
Pitx2	paired-like homeodomain transcription factor 2	803	18741	NM_011098
Pkd2l1	polycystic kidney disease 2-like 1	74881878	329064	NM_181422.2
Pkia	protein kinase inhibitor, alpha	805	18767	NM_008862
Pkig	protein kinase inhibitor, gamma	2483	18769	NM_011106
Pknox1	Pbx/knotted 1 homeobox	1401	18771	NM_016670
Pknox2	Pbx/knotted 1 homeobox 2	76135815	208076	NM_148950.1
Pkp2	plakophilin 2	73997149	67451	NM_026163.1
Pla2g12a	phospholipase A2, group XIIA	1518	66350	NM_023196
Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	74047841	27226	NM_013737.2
Plagl1	pleiomorphic adenoma gene-like 1	71249057	22634	NM_009538.1
Plcb1	phospholipase C, beta 1	75084969	18795	NM_019677.1
Plcb4	phospholipase C, beta 4	72008304	18798	NM_013829.1
Plcd1	phospholipase C, delta 1	1812	18799	NM_019676
Plcd3	phospholipase C, delta 3	276272	72469	NM_152813.1
Plcd3	phospholipase C, delta 3	77414915	72469	NM_152813.1
Plcl1	phospholipase C-like 1	75081396	227120	XM_129785.4
Plcl3	phospholipase C, eta 1	71717604	269437	NM_183191.1
Plcz1	phospholipase C, zeta 1	74988296	114875	NM_054066.2
Pld3	phospholipase D family, member 3	808	18807	NM_011116
Plek	pleckstrin	75084080	56193	NM_019549.1
Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	70743843	83436	NM_031257.2
Plekha5	pleckstrin homology domain containing, family A member 5	70743870	109135	NM_144920.2
Plekha7	pleckstrin homology domain containing, family A member 7	73992710	233765	NM_172743.1
Plekha1	pleckstrin homology domain containing, family B (evectins) member 1	71836842	27276	NM_013746.1
Plekhg1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	71670687	213783	XM_136911.4
Plekhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	74881855	269608	NM_001004156.1
Plekhh2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	74581448	213556	NM_177606.2
Plf	prolactin family 2, subfamily c, member 2	75077152	18811	NM_031191.1
Plg	plasminogen	2485	18815	NM_008877
Plk1	polo-like kinase 1 (Drosophila)	2487	18817	NM_011121
Plk2	polo-like kinase 2 (Drosophila)	74743272	20620	NM_152804.1
Pln	phospholamban	74357563	18821	NM_023129.3
Plp1	proteolipid protein (myelin) 1	69120553	18823	NM_011123.1
Plp1	proteolipid protein (myelin) 1	2489	18823	NM_011123
Pls3	plastin 3 (T-isoform)	355886	102866	NM_145629.1
Pltp	phospholipid transfer protein	74581394	18830	NM_011125.1

Plxdc1	plexin domain containing 1	814	72324	NM_028199
Plxdc2	plexin domain containing 2	74425563	67448	NM_026162.2
Plxna2	plexin A2	77280424	18845	NM_008882.1
Plxna2	plexin A2	70431431	18845	NM_008882.1
Plxna3	plexin A3	1403	18846	NM_008883
Plxna4	plexin A4	75084090	243743	NM_175750.2
Plxnb1	plexin B1	1561	235611	NM_172775
Plxnb2	plexin B2	1263	140570	XM_484491
Plxnb2	plexin B2	817	11666	XM_484491
Plxnb3	plexin B3	1265	140571	NM_019587
Plxnc1	plexin C1	820	54712	NM_018797
Plxnd1	plexin D1	73521005	67784	XM_149784.4
Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1	823	58801	NM_021451
Pmfbp1	polyamine modulated factor 1 binding protein 1	71717105	56523	NM_019938.1
Pmm1	phosphomannomutase 1	67936010	29858	NM_013872.1
Pmp22	peripheral myelin protein	825	18858	NM_008885
Pnck	pregnancy upregulated non-ubiquitously expressed CaM kinase	827	93843	NM_012040
Pnoc	prepronociceptin	75038402	18155	NM_010932.1
Pnrc1	proline-rich nuclear receptor coactivator 1	2501	108767	XM_131355
Pnrc2	proline-rich nuclear receptor coactivator 2	2491	52830	NM_026383
Podn	podocan	75988568	242608	NM_172874.2
Podxl2	podocalyxin-like 2	74047921	319655	NM_176973.3
Pofut2	protein O-fucosyltransferase 2	147	80294	NM_030262
Pogk	pogo transposable element with KRAB domain	71064277	71592	NM_175170.2
Pogz	pogo transposable element with ZNF domain	75651180	229584	NM_172683.1
Pola1	polymerase (DNA directed), alpha 1	75084100	18968	NM_008892.1
Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	74275101	66979	NM_025882.1
Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	75651230	66979	NM_025882.1
Polk	polymerase (DNA directed), kappa	75077171	27015	NM_012048.1
Polr1e	polymerase (RNA) I polypeptide E	75774108	64424	NM_022811.1
Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	72339344	66420	XM_282920.2
Pomc1	pro-opiomelanocortin-alpha	2493	18976	NM_008895
Pon3	paraoxonase 3	74357564	269823	NM_173006.1
Pop4	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	357096	66161	NM_025390.2
Pop4	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	77869859	66161	NM_025390.2
Postn	periostin, osteoblast specific factor	77371799	50706	NM_015784.1
Pou2f1	POU domain, class 2, transcription factor 1	1563	18986	NM_011137
Pou4f1	POU domain, class 4, transcription factor 1	74641304	18996	NM_011143.1
Pou6f1	POU domain, class 6, transcription factor 1	74357559	19009	NM_010127.2
Pou6f2	POU domain, class 6, transcription factor 2	71249067	218030	NM_175006.1
Ppap2a	phosphatidic acid phosphatase 2a	830	19012	NM_008247
Ppap2b	phosphatidic acid phosphatase type 2B	75749384	67916	NM_080555.1
Pparg	peroxisome proliferator activated receptor gamma	2495	19016	NM_011146
Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	74272480	67533	NM_026221.1
Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	2497	19042	NM_008910
Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	2499	14208	NM_008014
Ppm1l	protein phosphatase 1 (formerly 2C)-like	71924215	242083	NM_178726.1
Ppm2c	protein phosphatase 2C, magnesium dependent, catalytic subunit	74357581	381511	XM_355470.1
Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	73512186	18938	NM_008889.1

Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	75773706	58200	NM_021391.2
Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	73732146	19049	NM_144828.1
Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	73521813	66849	NM_025800.1
Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	75084111	244416	NM_177741.3
Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	832	66385	NM_023200
Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	71064176	243725	NM_181595.2
Ppp1r9b	protein phosphatase 1, regulatory subunit 9B	74271623	217124	NM_172261.2
Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	71836836	19052	NM_019411.2
Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	74882698	269643	NM_172994.2
Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	276265	19054	XM_356255.2
Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	77414925	19054	XM_356255.2
Ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform	74819327	225849	NM_198168.1
Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform	74047908	21770	NM_009358.2
Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	73817435	19055	NM_008913.1
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	32386	19058	NM_024459.1
Ppp3r2	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type II)	75084112	19059	NM_001004025.1
Ppp4r2	protein phosphatase 4, regulatory subunit 2	74511850	232314	NM_182939.1
Pqbp1	polyglutamine binding protein 1	1520	54633	NM_019478
Prcp	prolylcarboxypeptidase (angiotensinase C)	74819671	72461	NM_028243.1
Prdx1	peroxiredoxin 1	836	18477	NM_011034
Prdx3	peroxiredoxin 3	70743842	11757	NM_007452.1
Prdx4	peroxiredoxin 4	74819229	53381	NM_016764.1
Prdx5	peroxiredoxin 5	76115740	54683	NM_012021.1
Prdx6-rs1	peroxiredoxin 6, related sequence 1	74988306	320769	NM_177256.2
Prkacb	protein kinase, cAMP dependent, catalytic, beta	75043158	18749	NM_011100.3
Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	29	108099	NM_145401
Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	70616006	19085	NM_008923.2
Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	77332735	19087	NM_008924.1
Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	74583119	19088	NM_011158.2
Prkca	protein kinase C, alpha	840	18750	NM_011101
Prkca	protein kinase C, alpha	77869816	18750	NM_011101.1
Prkcb1	protein kinase C, beta 1	72129247	18751	NM_008855.1
Prkcc	protein kinase C, gamma	73521814	18752	NM_011102.2
Prkcd	protein kinase C, delta	70301274	18753	NM_011103.1
Prkch	protein kinase C, eta	73520406	18755	NM_008856.2
Prkcq	protein kinase C, theta	71670693	18761	NM_008859.1
Prkcq	protein kinase C, theta	77869867	18761	NM_008859.1
Prkcsh	protein kinase C substrate 80K-H	67870479	19089	NM_008925.1
Prkcsh	protein kinase C substrate 80K-H	77413682	19089	NM_008925.1
Prkcz	protein kinase C, zeta	841	18762	NM_008860
Prkdc	protein kinase, DNA activated, catalytic polypeptide	74882717	19090	NM_011159.1
Prkg1	protein kinase, cGMP-dependent, type I	73521817	19091	NM_011160.1
Prkg2	protein kinase, cGMP-dependent, type II	71670688	19092	NM_008926.2
Prlr	prolactin receptor	1268	19116	NM_011169
Prnp	prion protein	1405	19122	NM_011170
Prosapip1	ProSAPiP1 protein	71064051	241638	NM_197945.2
Prosc	proline synthetase co-transcribed	76115741	114863	NM_054057.1
Prox1	prospero-related homeobox 1	73520980	19130	NM_008937.2
Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	73907503	66921	NM_025845.1

Prph1	peripherin	70232000	19132	NM_013639.1
Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2	293663	212627	NM_144806.1
Prrg2	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	276063	65116	NM_022999.1
Prrx2	paired related homeobox 2	1522	20204	NM_009116
Prss12	protease, serine, 12 neurotrypsin (motopsin)	71836879	19142	NM_008939.1
Prss18	kallikrein related-peptidase 6	74988616	19144	NM_011177.1
Prss19	kallikrein related-peptidase 8	72129241	259277	NM_008940.1
Prss35	protease, serine, 35	74511839	244954	NM_178738.1
Psap	prosaposin	846	19156	NM_011179
Pscdbp	pleckstrin homology, Sec7 and coiled-coil domains, binding protein	1270	227929	NM_139200
Psd	pleckstrin and Sec7 domain containing	72128746	73728	NM_028627.2
Psg16	pregnancy specific glycoprotein 16	655307	26436	NM_007676.3
Psg16	pregnancy specific glycoprotein 16	77887858	26436	NM_007676.3
Psmb2	proteasome (prosome, macropain) subunit, beta type 2	74988552	26445	NM_011970.2
Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2	356850	19181	NM_011188.1
Psmc11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	74743282	69077	NM_178616.2
Psmc13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	74882718	23997	NM_011875.2
Psmc4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	2503	19185	NM_008951
Psmc5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	75146002	66998	NM_080554.1
Psme1	proteasome (prosome, macropain) 28 subunit, alpha	76115739	19186	NM_011189.1
Psme2	proteasome (prosome, macropain) 28 subunit, beta	74800893	19188	NM_011190.2
Pstpip1	proline-serine-threonine phosphatase-interacting protein 1	71717135	19200	NM_011193.1
Ptbp1	polypyrimidine tract binding protein 1	356857	19205	NM_008956.1
Ptcd1	pentatricopeptide repeat domain 1	74882764	71799	NM_133735.1
Ptcd2	pentatricopeptide repeat domain 2	293037	68927	XM_127497.3
Ptcd2	pentatricopeptide repeat domain 2	77414563	68927	XM_127497.3
Ptdss1	phosphatidylserine synthase 1	74800904	19210	NM_008959.2
Ptgds	prostaglandin D2 synthase (brain)	45667	19215	NM_008963.1
Ptgds	prostaglandin D2 synthase (brain)	655308	19215	NM_008963.1
Ptgds	prostaglandin D2 synthase (brain)	851	19215	NM_008963
Ptger4	prostaglandin E receptor 4 (subtype EP4)	1524	19219	NM_008965
Ptgfr	prostaglandin F receptor	72283795	19220	NM_008966.2
Ptgs1	prostaglandin-endoperoxide synthase 1	74800973	19224	NM_008969.1
Ptgs2	prostaglandin-endoperoxide synthase 2	71016664	19225	NM_011198.2
Pthlh	parathyroid hormone-like peptide	73592531	19227	NM_008970.1
Pthr1	parathyroid hormone receptor 1	2505	19228	NM_011199
Ptk2	PTK2 protein tyrosine kinase 2	75774672	14083	NM_007982.1
Ptk2b	PTK2 protein tyrosine kinase 2 beta	74357569	19229	NM_172498.1
Ptk7	PTK7 protein tyrosine kinase 7	74882765	71461	NM_175168.2
Ptk9l	twinfilin, actin-binding protein, homolog 2 (Drosophila)	73732148	23999	NM_011876.2
Ptn	pleiotrophin	2507	19242	NM_008973
Ptn	pleiotrophin	77866882	19242	NM_008973.1
Ptp4a1	protein tyrosine phosphatase 4a1	75079765	19243	NM_011200.1
Ptpn18	protein tyrosine phosphatase, non-receptor type 18	2509	19253	NM_011206
Ptpn2	protein tyrosine phosphatase, non-receptor type 2	77413686	19255	NM_008977.1
Ptpn3	protein tyrosine phosphatase, non-receptor type 3	74511860	19257	XM_355486.2
Ptpn4	protein tyrosine phosphatase, non-receptor type 4	74743283	19258	NM_019933.1
Ptpn5	protein tyrosine phosphatase, non-receptor type 5	74743293	19259	NM_013643.1
Ptpns1	signal-regulatory protein alpha	74583151	19261	NM_007547.1

Ptpcap	protein tyrosine phosphatase, receptor type, C polypeptide-associated protein	121091	19265	NM_016933.2
Ptpcd	protein tyrosine phosphatase, receptor type, D	855	19266	XM_131462
Ptpcj	protein tyrosine phosphatase, receptor type, J	73521803	19271	NM_008982.2
Ptpck	protein tyrosine phosphatase, receptor type, K	74743303	19272	NM_008983.1
Ptpcm	protein tyrosine phosphatase, receptor type, M	864	19274	NM_008984
Ptpco	protein tyrosine phosphatase, receptor type, O	72340109	19277	NM_011216.2
Ptpcr	protein tyrosine phosphatase, receptor type, R	74882784	19279	NM_011217.1
Ptpcs	protein tyrosine phosphatase, receptor type, S	74882787	19280	NM_011218.1
Ptpct	protein tyrosine phosphatase, receptor type, T	72008491	19281	NM_021464.1
Ptpct	protein tyrosine phosphatase, receptor type, T	866	19281	NM_021464
Ptpcu	protein tyrosine phosphatase, receptor type, U	858	19273	NM_011214
Ptpcv	protein tyrosine phosphatase, receptor type, V	73817436	13924	NM_007955.2
Ptpcz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1	77371825	19283	XM_358362.2
Ptrf	polymerase I and transcript release factor	73521818	19285	NM_008986.1
Pttg1	pituitary tumor-transforming 1	293036	30939	NM_013917.1
Pttg1ip	pituitary tumor-transforming 1 interacting protein	1956	108705	NM_145925
Purg	purine-rich element binding protein G	74882788	75029	NM_152821.1
Pus7	pseudouridylate synthase 7 homolog (S. cerevisiae)	77869776	78697	NM_178403.2
Pvalb	parvalbumin	69120565	19293	NM_013645.2
Pvalb	parvalbumin	868	19293	NM_013645
Pvr	poliovirus receptor	71670694	21332	NM_009310.1
Pvr	poliovirus receptor	119504	52118	NM_027514.1
Pvrl1	poliovirus receptor-related 1	74363351	58235	NM_021424.2
Pvrl3	poliovirus receptor-related 3	73521804	58998	NM_021495.1
Pvrl4	poliovirus receptor-related 4	2511	71740	XM_203738
Pwp2h	PWP2 periodic tryptophan protein homolog (yeast)	2513	110816	NM_029546
Pxn	paxillin	1814	19303	NM_011223
Pycl	pyrroline-5-carboxylate reductase-like	2515	66194	NM_025412
Pygb	brain glycogen phosphorylase	276075	110078	NM_153781.1
Qdpr	quinoid dihydropteridine reductase	75042261	110391	NM_024236.1
R74862	expressed sequence R74862	67936009	97423	NM_133790.1
Rab1	RAB1, member RAS oncogene family	878	19324	NM_008996
Rab12	RAB12, member RAS oncogene family	74988626	19328	NM_024448.1
Rab27b	RAB27b, member RAS oncogene family	74641314	80718	NM_030554.1
Rab37	RAB37, member of RAS oncogene family	73931643	58222	NM_021411.2
Rab3b	RAB3B, member RAS oncogene family	70436738	69908	NM_023537.4
Rab3c	RAB3C, member RAS oncogene family	73521805	67295	NM_023852.2
Rab3ip	RAB3A interacting protein	71717136	216363	NM_001003950.1
Rab6	RAB6, member RAS oncogene family	74047909	19346	NM_024287.2
Rab6ip1	Rab6 interacting protein 1	1526	19347	NM_021494
Rabep2	rabaptin, RAB GTPase binding effector protein 2	1970	70314	NM_030566
Rad23b	RAD23b homolog (S. cerevisiae)	881	19359	NM_009011
Rad51	RAD51 homolog (S. cerevisiae)	293471	19361	NM_011234.2
Raf1	v-raf-leukemia viral oncogene 1	1816	110157	NM_029780
Rai14	retinoic acid induced 14	73521806	75646	NM_030690.2
Rai17	zinc finger, MIZ-type containing 1	74988259	328365	NM_183208.2
Rai3	G protein-coupled receptor, family C, group 5, member A	199395	232431	NM_181444.3
Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	74657981	64143	NM_022327.3
Ramp1	receptor (calcitonin) activity modifying protein 1	1912	51801	NM_016894



Ramp3	receptor (calcitonin) activity modifying protein 3	1818	56089	NM_019511
Ran	RAN, member RAS oncogene family	2517	19384	NM_009391
Ranbp5	RAN binding protein 5	76115732	70572	NM_023579.2
Rangap1	RAN GTPase activating protein 1	2519	19387	NM_011241
Rap1b	RAS related protein 1b	74819347	215449	NM_024457.1
Rap1gds1	RAP1, GTP-GDP dissociation stimulator 1	654924	229877	NM_145544.1
Rap2b	RAP2B, member of RAS oncogene family	75934918	74012	NM_028712.3
Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	74749895	56508	NM_019688.1
Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5	70301084	217944	NM_175930.2
Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	75041528	192786	XM_484024.1
Rara	retinoic acid receptor, alpha	1528	19401	NM_009024
Rarb	retinoic acid receptor, beta	75038442	218772	NM_011243.1
Rarg	retinoic acid receptor, gamma	130913	19411	NM_011244.2
Rarres1	retinoic acid receptor responder (tazarotene induced) 1	75084131	109222	XM_130987.4
Rarres2	retinoic acid receptor responder (tazarotene induced) 2	75077281	71660	NM_027852.1
Rasa4	RAS p21 protein activator 4	74425552	54153	XM_355650.2
Rasal1	RAS protein activator like 1 (GAP1 like)	75774111	19415	NM_013832.2
Rasal2	RAS protein activator like 2	75147758	226525	XM_355247.3
Rasd1	RAS, dexamethasone-induced 1	2521	19416	NM_009026
Rasd2	RASD family, member 2	73636089	75141	XM_204287.4
Rasgef1b	RasGEF domain family, member 1B	71358553	320292	NM_145839.1
Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	1274	19417	NM_011245
Rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2	73992916	19418	NM_009027.2
Rasgrp1	RAS guanyl releasing protein 1	76115742	19419	NM_011246.2
Rasgrp2	RAS, guanyl releasing protein 2	76115743	19395	NM_011242.1
Rasgrp4	RAS guanyl releasing protein 4	76135807	233046	NM_145149.1
Ras11a	RAS-like, family 11, member A	75988636	68895	XM_485698.1
Ras11b	RAS-like, family 11, member B	71717137	68939	XM_355606.2
Rassf3	Ras association (RalGDS/AF-6) domain family 3	71836799	192678	NM_138956.2
Rassf4	Ras association (RalGDS/AF-6) domain family 4	74988636	213391	NM_178045.3
Rassf6	Ras association (RalGDS/AF-6) domain family 6	75041561	73246	XM_132163.5
Rax	retina and anterior neural fold homeobox	1820	19434	NM_013833
Rb1cc1	RB1-inducible coiled-coil 1	75043159	12421	NM_009826.3
Rbbp6	retinoblastoma binding protein 6	170	19647	NM_011247
Rbed1	RNA binding motif and ELMO domain 1	75042257	232089	NM_144917.2
Rbm11	RNA binding motif protein 11	1411	224344	NM_198302
Rbm18	RNA binding motif protein 18	356083	67889	NM_026434.2
Rbm19	RNA binding motif protein 19	71016585	74111	NM_028762.1
Rbm4	RNA binding motif protein 4	888	19653	NM_009032
Rbmx	RNA binding motif protein, X chromosome	75043154	19655	NM_011252.2
Rbp4	retinol binding protein 4, plasma	71016583	19662	NM_011255.1
Rbpms2	RNA binding protein with multiple splicing 2	73512496	71973	NM_028030.2
Rcn1	reticulocalbin 1	73788083	19672	NM_009037.1
Rcn1	reticulocalbin 1	73788084	19672	NM_009037.1
Rcn2	reticulocalbin 2	73997151	26611	NM_011992.1
Rcor1	REST corepressor 1	74819517	217864	NM_198023.1
Rcsd1	RCSD domain containing 1	75934525	226594	NM_178593.2
Rdh14	retinol dehydrogenase 14 (all-trans and 9-cis)	75043157	105014	NM_023697.1
Rdh5	retinol dehydrogenase 5	75042255	19682	NM_134006.3

Rec8L1	REC8 homolog (yeast)	77278975	56739	NM_020002.2
Recql4	RecQ protein-like 4	75084132	79456	NM_058214.1
Recql5	RecQ protein-like 5	75079799	170472	NM_130454.1
Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	2523	19697	NM_009045
Relb	avian reticuloendotheliosis viral (v-rel) oncogene related B	2525	19698	NM_009046
Reln	reelin	890	19699	NM_011261
Reps2	RALBP1 associated Eps domain containing protein 2	76135799	194590	NM_178256.2
Rer1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	323586	67830	NM_026395.1
Resp18	regulated endocrine-specific protein 18	71015810	19711	NM_009049.1
Rfc5	replication factor C (activator 1) 5	74882798	72151	XM_132348.3
Rfk	riboflavin kinase	71064080	54391	NM_019437.1
Rfrp	neuropeptide VF precursor	74882808	60531	NM_021892.1
Rfwd2	ring finger and WD repeat domain 2	75080751	26374	NM_011931.1
Rfx1	regulatory factor X, 1 (influences HLA class II expression)	895	19724	NM_009055
Rfx1	regulatory factor X, 1 (influences HLA class II expression)	77371867		NM_009055.2
Rfx3	regulatory factor X, 3 (influences HLA class II expression)	70634235	19726	NM_011265.2
Rfx4	regulatory factor X, 4 (influences HLA class II expression)	71249068	71137	NM_027689.1
Rfxank	regulatory factor X-associated ankyrin-containing protein	67881545	19727	NM_011266.1
Rga	recombination activating gene 1 activating protein 1	67870478	19729	NM_009057.1
Rgag1	retrotransposon gag domain containing 1	75041526	209540	XM_142197.3
Rgnef	Rho-guanine nucleotide exchange factor	74272892	110596	NM_012026.1
Rgs10	regulator of G-protein signalling 10	74511849	67865	NM_026418.1
Rgs12	regulator of G-protein signaling 12	70613990	71729	NM_173402.1
Rgs14	regulator of G-protein signaling 14	2529	51791	NM_016758
Rgs16	regulator of G-protein signaling 16	1567	19734	NM_011267
Rgs19	regulator of G-protein signaling 19	1530	56470	NM_026446
Rgs19ip1	GIPC PDZ domain containing family, member 1	67755429	67903	NM_018771.3
Rgs2	regulator of G-protein signaling 2	73635771	19735	NM_009061.2
Rgs20	regulator of G-protein signaling 20	73817437	58175	NM_021374.1
Rgs3	regulator of G-protein signaling 3	1822	50780	NM_019492
Rgs4	regulator of G-protein signaling 4	74511884	19736	NM_009062.2
Rgs4	regulator of G-protein signaling 4	1569	19736	NM_009062
Rgs5	regulator of G-protein signaling 5	74357571	19737	NM_009063.2
Rgs6	regulator of G-protein signaling 6	74272893	50779	NM_015812.1
Rgs9	regulator of G-protein signaling 9	73521819	19739	NM_011268.1
Rhbdf1	rhomboid family 1 (Drosophila)	2533	13650	NM_010117
Rho	rhodopsin	1824	212541	NM_145383
Rhobtb3	Rho-related BTB domain containing 3	74583162	73296	NM_028493.1
Rims3	regulating synaptic membrane exocytosis 3	74512027	242662	NM_182929.1
Rin1	Ras and Rab interactor 1	67870468	225870	NM_145495.1
Rkhd1	mex3 homolog D (C. elegans)	75041562	237400	NM_198615.1
Rln3	relaxin 3	73929581	212108	NM_173184.1
Rnasel	ribonuclease L (2', 5'-oligoadenylate synthetase-dependent)	73817438	24014	NM_011882.1
Rnaset2	ribonuclease T2B	74988459	68195	NM_026611.1
Rnf10	ring finger protein 10	67936005	50849	NM_016698.1
Rnf11	ring finger protein 11	1276	29864	NM_013876
Rnf122	ring finger protein 122	275875	68867	NM_175136.1
Rnf128	ring finger protein 128	1914	66889	NM_023270
Rnf134	polycomb group ring finger 6	70634297	71041	NM_027654.1

Rnf149	ring finger protein 149	898	67702	XM_129803
Rnf152	ring finger protein 152	75043151	320311	NM_178779.2
Rnf19	ring finger protein 19A	73931414	30945	NM_013923.1
Rnf32	ring finger protein 32	75080209	56874	NM_021470.3
Rnh1	ribonuclease/angiogenin inhibitor 1	74800925	107702	NM_145135.2
Rnpc1	RNA binding motif protein 38	2535	56190	NM_019547
Robo1	roundabout homolog 1 (Drosophila)	73521820	19876	NM_019413.1
Robo2	roundabout homolog 2 (Drosophila)	75080998	268902	NM_175549.2
Rock2	Rho-associated coiled-coil containing protein kinase 2	75988621	19878	Mm.25117.0
Rora	RAR-related orphan receptor alpha	2537	19883	NM_013646
Rora	RAR-related orphan receptor alpha	900	19883	NM_013646
Rora	RAR-related orphan receptor alpha	77371865	19883	NM_013646.1
Rorb	RAR-related orphan receptor beta	2539	225998	NM_146095
Rorc	RAR-related orphan receptor gamma	67855412	19885	NM_011281.1
Rpgr	retinitis pigmentosa GTPase regulator	67936211	19893	NM_011285.1
Rph3a	rabphilin 3A	71587899	19894	NM_011286.2
Rpl11	ribosomal protein L11	276067	67025	NM_025919.1
Rpl15	ribosomal protein L15	74882810	66480	NM_025586.1
Rpl21	ribosomal protein L21	74882831	19933	NM_019647.3
Rpl23	ribosomal protein L23	74819237	65019	NM_022891.1
Rpl32	ribosomal protein L32	75934920	19951	NM_172086.1
Rpl8	ribosomal protein L8	74749928	26961	NM_012053.1
Rpn1	ribophorin I	75774675	103963	NM_133933.2
Rpn2	ribophorin II	906	20014	NM_019642
Rpo2tc1	SUB1 homolog (S. cerevisiae)	356490	20024	NM_011294.2
Rpp25	ribonuclease P 25 subunit (human)	75146006	102614	NM_133982.1
Rprm	reprimin, TP53 dependent G2 arrest mediator candidate	75651169	67874	NM_023396.3
Rprm	reprimin, TP53 dependent G2 arrest mediator candidate	71836875	67874	NM_023396.3
Rps12	ribosomal protein S12	70928395	20042	NM_011295.2
Rps15	ribosomal protein S15	75774687	20054	NM_009091.1
Rps15a	ribosomal protein S15a	74357560	267019	NM_170669.2
Rps19	ribosomal protein S19	72081492	20085	NM_023133.1
Rps21	ribosomal protein S21	74425523	66481	NM_025587.1
Rps5	ribosomal protein S5	907	20103	NM_009095
Rps5	ribosomal protein S5	77868800	20103	NM_009095.1
Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	70301276	20112	NM_011299.3
Rps6ka3	ribosomal protein S6 kinase polypeptide 3	71670727	110651	NM_148945.1
Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	1976	73086	NM_153587
Rrad	Ras-related associated with diabetes	75080239	56437	NM_019662.1
Rragd	Ras-related GTP binding D	73929582	52187	NM_027491.1
Rrm2	ribonucleotide reductase M2	74272039	20135	NM_009104.1
Rsnl2	CAP-GLY domain containing linker protein family, member 4	75774680	78785	NM_030179.2
Rspo1	R-spondin homolog (Xenopus laevis)	73636101	192199	NM_138683.1
Rtl1	retrotransposon-like 1	74988325	353326	NM_184109.1
Rtn1	reticulin 1	70928293	104001	NM_153457.4
Rtn2	reticulin 2 (Z-band associated protein)	909	20167	NM_013648
Rtn3	reticulin 3	83161	20168	NM_001003930.1
Rtn4	reticulin 4	70805906	68585	NM_024226.2
Rtn4r	reticulin 4 receptor	72080145	65079	NM_022982.1

Rtn4rl1	reticulon 4 receptor-like 1	1826	237847	NM_177708
Rtn4rl2	reticulon 4 receptor-like 2	74581375	269295	NM_199223.1
Runx2	runt related transcription factor 2	1278	12393	NM_009820
Rutbc2	small G protein signaling modulator 1	73521821	52850	NM_172718.1
Rutbc3	small G protein signaling modulator 3	67870081	105835	NM_134091.1
Rwdd2	RWD domain containing 2A	74511895	69519	NM_027100.1
Rxrb	retinoid X receptor beta	1916	20182	NM_011306
Rxrg	retinoid X receptor gamma	917	20183	NM_009107
Ryk	receptor-like tyrosine kinase	2541	20187	NM_013649
Ryr1	ryanodine receptor 1, skeletal muscle	71247657	20190	NM_009109.1
S100a10	S100 calcium binding protein A10 (calpactin)	70560277	20194	NM_009112.1
S100a16	S100 calcium binding protein A16	77371787	67860	NM_026416.2
S100a6	S100 calcium binding protein A6 (calcyclin)	77278967	20200	NM_011313.1
S100b	S100 protein, beta polypeptide, neural	923	20203	NM_009115
Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	74882832	83493	NM_030692.1
Sall3	sal-like 3 (Drosophila)	74363352	20689	NM_178280.3
Samd11	sterile alpha motif domain containing 11	70928360	231004	NM_173736.2
Samsn1	SAM domain, SH3 domain and nuclear localization signals, 1	925	67742	NM_023380
Sara1	SAR1 gene homolog A (S. cerevisiae)	321204	20224	NM_009120.1
Sart3	squamous cell carcinoma antigen recognized by T-cells 3	74819691	53890	NM_016926.1
Sash1	SAM and SH3 domain containing 1	71924225	70097	NM_175155.3
Satb1	special AT-rich sequence binding protein 1	2545	20230	NM_009122
Satb1	special AT-rich sequence binding protein 1	927	20230	NM_009122
Satb2	special AT-rich sequence binding protein 2	73992708	212712	NM_139146.1
Sbf1	SET binding factor 1	276264	77980	XM_358316.2
Sbk1	SH3-binding kinase 1	71836807	104175	NM_145587.1
Sbno1	sno, strawberry notch homolog 1 (Drosophila)	930	243272	XM_355637
Sc4mol	sterol-C4-methyl oxidase-like	74750020	66234	NM_025436.1
Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae)	227160	235293	NM_172769.1
Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae)	77414164	235293	NM_172769.1
Sca1	ataxin 1	932		NM_009124
Sca10	ataxin 10	544899	54138	NM_016843.1
Scand1	SCAN domain-containing 1	2549	19018	NM_020255
Scara3	scavenger receptor class A, member 3	75042270	219151	NM_172604.1
Scarb1	scavenger receptor class B, member 1	2551	20778	NM_016741
Scarb2	scavenger receptor class B, member 2	72081482	12492	NM_007644.2
Sccpdh	saccharopine dehydrogenase (putative)	73635772	109232	NM_178653.2
Scd1	stearoyl-Coenzyme A desaturase 1	71836746	20249	NM_009127.2
Scd2	stearoyl-Coenzyme A desaturase 2	74819250	20250	NM_009128.1
Scd3	stearoyl-coenzyme A desaturase 3	74882915	30049	NM_024450.1
Scg2	secretogranin II	934	20254	NM_009129
Scg3	secretogranin III	73718057	20255	NM_009130.1
Scg5	secretogranin V	75773511	20394	NM_009162.2
Scgf	C-type lectin domain family 11, member a	2553		NM_009131
Schip1	schwannomin interacting protein 1	72077455	30953	NM_013928.2
Scml2	sex comb on midleg-like 2 (Drosophila)	73992917	107815	NM_133194.2
Scml4	sex comb on midleg-like 4 (Drosophila)	75147763	268297	NM_172938.2
Scn1a	sodium channel, voltage-gated, type I, alpha	77340528	20265	XM_619757.1
Scn3b	sodium channel, voltage-gated, type III, beta	71064082	235281	NM_153522.1

Scn4b	sodium channel, type IV, beta	73636111	399548	XM_357946.2
Scn5a	sodium channel, voltage-gated, type V, alpha	73907501	20271	NM_021544.1
Scnn1a	sodium channel, nonvoltage-gated, type I, alpha	70562125	20276	NM_011324.1
Scnn1g	sodium channel, nonvoltage-gated 1 gamma	1918	20278	NM_011326
Scrg1	scrapie responsive gene 1	71924331	20284	NM_009136.2
Scrn1	secernin 1	74357551	69938	NM_027268.1
Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	73636035	170729	NM_130893.2
Scube1	signal peptide, CUB domain, EGF-like 1	74272894	64706	NM_022723.1
Scube2	signal peptide, CUB domain, EGF-like 2	71924235	56788	NM_020052.1
Scube3	signal peptide, CUB domain, EGF-like 3	74988656	268935	NM_001004366.1
Sdc2	syndecan 2	72080155	15529	NM_008304.1
Sdc3	syndecan 3	71358662	20970	NM_011520.2
Sdcbp	syndecan binding protein	70744518	53378	NM_016807.1
Sdccag33	teashirt zinc finger family member 1	72129289	110796	XM_129060.4
Sdccag33l	teashirt zinc finger family member 2	72129294	228911	XM_130644.5
Sdccag8	serologically defined colon cancer antigen 8	323593	76816	NM_029756.1
Sdfr2	sidekick homolog 2 (chicken)	2557	237979	NM_009146
Sdhb	succinate dehydrogenase complex, subunit B, iron sulfur (lp)	74658140	67680	NM_023374.3
Sdk2	sidekick homolog 2 (chicken)	77332746	237979	NM_172800.2
Sec14l1	SEC14-like 1 (S. cerevisiae)	74988453	74136	NM_028777.1
Sec15l1	exocyst complex component 6	73817986	107371	NM_175353.1
Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)	356853	57743	NM_021305.2
Sec8l1	exocyst complex component 4	74658239	20336	NM_009148.1
Selk	selenoprotein K	74800903	80795	NM_019979.1
Selpl	selectin, platelet (p-selectin) ligand	74988637	20345	NM_009151.2
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	73592528	20346	NM_009152.2
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	937	20346	NM_009152
Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	939	20348	NM_013657
Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	74581376	108151	NM_028882.2
Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	70436736	20349	NM_011348.1
Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	72007563	20350	NM_011349.2
Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 942		20351	NM_013658
Sema4d	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 945		20354	NM_013660
Sema4g	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 71587856		26456	NM_011976.1
Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 950		20356	NM_009154
Sema5b	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 953		20357	NM_013661
Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	71358651	20358	NM_018744.1
Sema6c	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	75080151	20360	NM_011351.1
Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	74750032	214968	NM_172537.2
Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	955	20361	NM_011352
Senp2	SUMO/sentrin specific peptidase 2	276274	75826	NM_029457.2
Serinc1	serine incorporator 1	77413696	56442	NM_019760.1
Serinc5	serine incorporator 5	77278973	218442	NM_172588.2
Serpina1e	serine (or cysteine) peptidase inhibitor, clade A, member 1e	75084134	20704	NM_009247.1
Serpina3c	serine (or cysteine) peptidase inhibitor, clade A, member 3C	74511905	16625	NM_008458.1
Serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K	72081514	20714	NM_011458.1
Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	75043155	20716	NM_009252.1
Serpina9	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 9	71670728	71907	NM_027997.1
Serpinb1b	serine (or cysteine) peptidase inhibitor, clade B, member 1b	544327	282663	NM_173052.1

Serpinb1c	serine (or cysteine) peptidase inhibitor, clade B, member 1c	74511967	380839	NM_173051.1
Serpinb2	serine (or cysteine) peptidase inhibitor, clade B, member 2	75084144	18788	NM_011111.3
Serpinb6a	serine (or cysteine) peptidase inhibitor, clade B, member 6a	74425564	20719	NM_009254.2
Serpinb8	serine (or cysteine) peptidase inhibitor, clade B, member 8	293668	20725	NM_011459.2
Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	74047768	20720	NM_009255.2
Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	2559	20317	NM_011340
Serpin1	serine (or cysteine) peptidase inhibitor, clade I, member 1	963	20713	NM_009250
Sertad4	SERTA domain containing 4	71920519	214791	NM_198247.1
Sesn1	sestrin 1	70231304	140742	XM_125538.4
Set7	SET domain containing (lysine methyltransferase) 7	71016630	73251	NM_080793.2
Setbp1	SET binding protein 1	1532	240427	NM_053099
Sez6	seizure related gene 6	71063725	20370	NM_021286.2
Sez6l	seizure related 6 homolog like	73929583	56747	XM_132255.6
Sez6l2	seizure related 6 homolog like 2	1407	233878	NM_144926
Sf3a2	splicing factor 3a, subunit 2	74882916	20222	NM_013651.3
Sf3b2	splicing factor 3b, subunit 2	74988735	319322	NM_030109.1
Sfmbt2	Scm-like with four mbt domains 2	73929593	353282	NM_177386.2
Sfn	stratifin	2561	55948	NM_018754
Sfpi1	SFFV proviral integration 1	227535	20375	NM_011355.1
Sfrp1	secreted frizzled-related protein 1	2563	20377	NM_013834
Sfrp2	secreted frizzled-related protein 2	1830	20319	NM_009144
Sfrs9	splicing factor, arginine/serine rich 9	75043152	108014	NM_025573.2
Sgcd	sarcoglycan, delta (dystrophin-associated glycoprotein)	71717142	24052	NM_011891.2
Sgcg	sarcoglycan, gamma (dystrophin-associated glycoprotein)	74749941	24053	NM_011892.1
Sgcz	sarcoglycan zeta	74749942	244431	NM_145841.1
Sgk3	serum/glucocorticoid regulated kinase 3	75650862	170755	NM_133220.1
Sgtb	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	71924341	218544	NM_144838.1
Sh3bgr	SH3-binding domain glutamic acid-rich protein	1416	50795	NM_015825
Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2	71717686	212531	NM_172507.2
Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2	77887860	212531	NM_172507.2
Sh3bp4	SH3-domain binding protein 4	75774110	98402	NM_133816.1
Sh3d19	SH3 domain protein D19	74425516	27059	NM_012059.2
Sh3gl2	SH3-domain GRB2-like 2	74581397	20404	NM_019535.2
Sh3kbp1	SH3-domain kinase binding protein 1	74272906	58194	NM_021389.3
Sh3md2	SH3 domain containing ring finger 1	74581451	59009	NM_021506.1
Sh3px3	SH3 and PX domain containing 3	74882525	235406	NM_175483.2
Sh3rf2	SH3 domain containing ring finger 2	71670729	269016	NM_172966.1
Shb	src homology 2 domain-containing transforming protein B	71670695	230126	XM_131399.5
Shh	sonic hedgehog	1418	20423	NM_009170
Shhrs		2000		XM_489124
Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	73519850	56392	NM_019658.2
Siat6	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	2567		NM_009176
Siglech	sialic acid binding Ig-like lectin H	77332094	233274	NM_178706.2
Siglecl1	sialic acid binding Ig-like lectin E	1832		NM_031181
Sim1	single-minded homolog 1 (Drosophila)	72338698	20464	NM_011376.1
Sipa111	signal-induced proliferation-associated 1 like 1	74511986	217692	NM_172579.1
Sipa112	signal-induced proliferation-associated 1 like 2	72118960	244668	XM_146572.4
Sirt2	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	75651224	64383	NM_022432.2
Six1	sine oculis-related homeobox 1 homolog (Drosophila)	1834	20471	NM_009189

Six3os1	Six3 opposite strand transcript 1	75041431	77868	NM_175267.2
Skiv2l2	superkiller viralicidic activity 2-like 2 ( <i>S. cerevisiae</i> )	322964	72198	NM_028151.1
Slc	src-like adaptor	2569	20491	NM_009192
Slc2b	exophilin 5	75080619	320051	NM_176846.2
Slc10a3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	74047876	214601	NM_145406.1
Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	2571	18174	NM_008732
Slc12a2	solute carrier family 12, member 2	74882926	20496	NM_009194.1
Slc12a3	solute carrier family 12, member 3	2573	20497	NM_019415
Slc12a8	solute carrier family 12 (potassium/chloride transporters), member 8	1836	171286	NM_134251
Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	2575	114644	NM_054055
Slc16a14	solute carrier family 16 (monocarboxylic acid transporters), member 14	2577	71781	NM_027921
Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), member 2	73929597	20502	NM_009197.1
Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	72080085	80879	NM_030696.2
Slc16a4	solute carrier family 16 (monocarboxylic acid transporters), member 4	2579	229699	NM_146136
Slc16a6	solute carrier family 16 (monocarboxylic acid transporters), member 6	2581	104681	NM_134038
Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	73818754	140919	NM_080853.2
Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	75081210	72961	NM_182993.1
Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	70436317	72961	NM_182993.1
Slc17a8	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 8	71587918	216227	NM_182959.2
Slc18a1	solute carrier family 18 (vesicular monoamine), member 1	2583	110877	NM_153054
Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	967	214084	NM_013031
Slc18a3	solute carrier family 18 (vesicular monoamine), member 3	73521822	20508	NM_021712.1
Slc19a1	solute carrier family 19 (sodium/hydrogen exchanger), member 1	1282	20509	NM_031196
Slc19a2	solute carrier family 19 (thiamine transporter), member 2	2585	116914	NM_054087
Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	71836888	20510	NM_009199.1
Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	73521823	20511	NM_011393.1
Slc20a1	solute carrier family 20, member 1	1571	20515	NM_015747
Slc20a2	solute carrier family 20, member 2	70231308	20516	NM_011394.1
Slc22a13	solute carrier family 22 (organic cation transporter), member 13	1663	102570	NM_133980
Slc22a3	solute carrier family 22 (organic cation transporter), member 3	73931644	20519	NM_011395.1
Slc22a7	solute carrier family 22 (organic anion transporter), member 7	227162	108114	NM_144856.1
Slc22a8	solute carrier family 22 (organic anion transporter), member 8	74657924	19879	NM_031194.2
Slc24a2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	71924238	76376	NM_172426.1
Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	70927810	94249	NM_053195.1
Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	2587	13358	NM_153150
Slc25a10	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	74047855	27376	NM_013770.1
Slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	2589	67863	NM_024211
Slc25a22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	1639	68267	NM_026646
Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	544516	227731	NM_146118.2
Slc25a27	solute carrier family 25, member 27	74988334	74011	NM_028711.1
Slc25a3	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	972	18674	NM_133668
Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	2591	11740	NM_007451
Slc26a7	solute carrier family 26, member 7	2595	208890	NM_145947
Slc26a8	solute carrier family 26, member 8	2597	224661	NM_146076
Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	75651228	26457	NM_011977.2
Slc27a4	solute carrier family 27 (fatty acid transporter), member 4	1920	26569	NM_011989
Slc28a3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	70927425	114304	NM_022317.2
Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	1838	63959	NM_022880
Slc29a4	solute carrier family 29 (nucleoside transporters), member 4	67862430	243328	NM_146257.1

Slc29a4	solute carrier family 29 (nucleoside transporters), member 4	77414149	243328	NM_146257.1
Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	74882936	20525	NM_011400.1
Slc2a12	solute carrier family 2 (facilitated glucose transporter), member 12	74581449	353169	NM_178934.2
Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	1840	20527	NM_011401
Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	2599	20528	NM_009204
Slc2a6	solute carrier family 2 (facilitated glucose transporter), member 6	71670696	227659	NM_172659.1
Slc30a3	solute carrier family 30 (zinc transporter), member 3	73788094	22784	NM_011773.1
Slc30a3	solute carrier family 30 (zinc transporter), member 3	73788095	22784	NM_011773.1
Slc31a1	solute carrier family 31, member 1	2603	20529	NM_175090
Slc31a2	solute carrier family 31, member 2	75773700	20530	NM_025286.1
Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	72081554	22348	NM_009508.1
Slc34a1	solute carrier family 34 (sodium phosphate), member 1	1842	20505	NM_011392
Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member 1	2605	24060	NM_011895
Slc35a2	solute carrier family 35 (UDP-galactose transporter), member A2	2607	22232	NM_078484
Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	2609	229782	NM_144902
Slc35a4	solute carrier family 35, member A4	2611	67843	NM_026404
Slc35b1	solute carrier family 35, member B1	2613	110172	XM_128634
Slc35b4	solute carrier family 35, member B4	75774107	58246	NM_021435.1
Slc35c2	solute carrier family 35, member C2	2615	228875	NM_144893
Slc35d3	solute carrier family 35, member D3	73929607	76157	XM_125515.4
Slc35f1	solute carrier family 35, member F1	75084145	215085	NM_178675.3
Slc35f2	solute carrier family 35, member F2	74819683	72022	NM_028060.2
Slc35f3	solute carrier family 35, member F3	75084156	210027	NM_175434.2
Slc36a1	solute carrier family 36 (proton/amino acid symporter), member 1	75041491	215335	NM_153139.3
Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2	1069	246049	NM_153170
Slc36a4	solute carrier family 36 (proton/amino acid symporter), member 4	1597	234967	NM_172289
Slc38a1	solute carrier family 38, member 1	75988508	105727	NM_134086.2
Slc38a1	solute carrier family 38, member 1	1844	105727	NM_134086
Slc38a3	solute carrier family 38, member 3	70436729	76257	NM_023805.2
Slc38a4	solute carrier family 38, member 4	2617	69354	NM_027052
Slc39a14	solute carrier family 39 (zinc transporter), member 14	1846	213053	NM_144808
Slc39a3	solute carrier family 39 (zinc transporter), member 3	2619	106947	NM_134135
Slc39a5	solute carrier family 39 (metal ion transporter), member 5	76135744	72002	NM_028051.1
Slc39a5	solute carrier family 39 (metal ion transporter), member 5	1645	72002	NM_028051
Slc39a6	solute carrier family 39 (metal ion transporter), member 6	73930852	106957	NM_139143.1
Slc41a3	solute carrier family 41, member 3	73512484	71699	XM_132686.4
Slc43a2	solute carrier family 43, member 2	74425544	215113	NM_173388.1
Slc44a1	solute carrier family 44, member 1	77925099	100434	NM_133891.2
Slc4a10	solute carrier family 4, sodium bicarbonate cotransporter-like, member 10	1922	94229	NM_033552
Slc4a2	solute carrier family 4 (anion exchanger), member 2	74583129	20535	NM_009207.1
Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	2621	20537	NM_019810
Slc5a3	solute carrier family 5 (inositol transporters), member 3	976	53881	NM_017391
Slc5a7	solute carrier family 5 (choline transporter), member 7	73929608	63993	NM_022025.3
Slc6a1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	476	232333	NM_178703
Slc6a15	solute carrier family 6 (neurotransmitter transporter), member 15	73929609	103098	NM_175328.1
Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	73615562	20538	NM_009209.2
Slc6a20	solute carrier family 6 (neurotransmitter transporter), member 20	77371783	22599	NM_011731.2
Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	978	13162	NM_010020
Slc6a4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	2623	15567	NM_010484



Slc6a5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	73771232	104245	NM_148931.2
Slc6a5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	73771231	104245	NM_148931.2
Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	1850	21366	NM_009320
Slc6a7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	71016653	240332	NM_201353.1
Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	1420	14664	NM_008135
Slc7a3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	73817929	11989	NM_007515.1
Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	293662	330836	NM_178798.2
Slc8a1	solute carrier family 8 (sodium/calcium exchanger), member 1	73521807	20541	NM_011406.1
Slc8a2	solute carrier family 8 (sodium/calcium exchanger), member 2	74581450	110891	NM_148946.2
Slc8a3	solute carrier family 8 (sodium/calcium exchanger), member 3	74357546	110893	NM_080440.1
Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	72080207	20544	NM_016981.1
Slc9a2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	74749943	226999	XM_129721.4
Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	74657980	65962	NM_023449.1
Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	76115744	236794	NM_172780.1
Slc9a7	solute carrier family 9 (sodium/hydrogen exchanger), isoform 7	77278977	236727	NM_177353.2
Slc9a8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	1852	77031	NM_148929
Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), isoform 9	71670730	331004	NM_177909.2
Slco1a5	solute carrier organic anion transporter family, member 1a5	67850945	108096	NM_130861.1
Slco3a1	solute carrier organic anion transporter family, member 3a1	293691	108116	NM_023908.1
Slco4a1	solute carrier organic anion transporter family, member 4a1	2625	108115	NM_148933
Slit1	slit homolog 1 (Drosophila)	73788105	20562	NM_015748.1
Slit1	slit homolog 1 (Drosophila)	73788106	20562	NM_015748.1
Slit2	slit homolog 2 (Drosophila)	980	20563	NM_178804
Slit3	slit homolog 3 (Drosophila)	73929858	20564	XM_203363.4
Slitrk1	SLIT and NTRK-like family, member 1	74882937	76965	NM_199065.1
Slitrk4	SLIT and NTRK-like family, member 4	74882938	245446	NM_178740.3
Slitrk6	SLIT and NTRK-like family, member 6	73992918	239250	NM_175499.2
Sln	sarcophilin	74425522	66402	NM_025540.1
Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	76085747	67155	NM_011416.2
Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	1972	67155	NM_011416
Smoc1	SPARC related modular calcium binding 1	71717592	64075	NM_022316.1
Smoc2	SPARC related modular calcium binding 2	74357576	64074	NM_022315.1
Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	67881552	20597	NM_011421.1
Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	77413684	20597	NM_011421.1
Sms	spermine synthase	74819260	20603	NM_009214.2
Smtn	smoothelin	74819233	29856	NM_013870.1
Smu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	74819686	74255	NM_021535.2
Smug1	single-strand selective monofunctional uracil DNA glycosylase	73992919	71726	NM_027885.2
Snap25	synaptosomal-associated protein 25	1854	20614	NM_011428
Snap91	synaptosomal-associated protein 91	984	20616	NM_013669
Snapc2	small nuclear RNA activating complex, polypeptide 2	77280343	102209	NM_133968.1
Snca	synuclein, alpha	989	20617	NM_009221
Snca	synuclein, alpha	986	20617	NM_009221
Sncg	synuclein, gamma	72081426	20618	NM_011430.1
Sned1	sushi, nidogen and EGF-like domains 1	74958587	208777	NM_172463.3
Sntb1	syntrophin, basic 1	71670741	20649	NM_016667.1
Snx25	sorting nexin 25	73929868	102141	XM_134171.4
Snx26	sorting nexin 26	74583174	233071	NM_178252.2
Soat2	sterol O-acyltransferase 2	74425515	223920	NM_146064.1

Socs5	suppressor of cytokine signaling 5	74274685	56468	NM_019654.2
Socs6	suppressor of cytokine signaling 6	70634236	54607	NM_018821.2
Sod1	superoxide dismutase 1, soluble	994	20655	NM_011434
Sod3	superoxide dismutase 3, extracellular	74273308	20657	NM_011435.2
Son	Son cell proliferation protein	996	20658	NM_019973
Sorbs1	sorbin and SH3 domain containing 1	74425572	20411	NM_009166.1
Sorcs1	VPS10 domain receptor protein SORCS 1	74800882	58178	NM_021377.1
Sorcs2	sortilin-related VPS10 domain containing receptor 2	74047717	81840	NM_030889.1
Sorcs3	sortilin-related VPS10 domain containing receptor 3	75988635	66673	NM_025696.1
Sorl1	sortilin-related receptor, LDLR class A repeats-containing	74511924	20660	NM_011436.1
Sostdc1	sclerostin domain containing 1	71836808	66042	NM_025312.1
Sostdc1	sclerostin domain containing 1	77874602	66042	NM_025312.1
Sox10	SRY-box containing gene 10	119502	20665	XM_128139.2
Sox11	SRY-box containing gene 11	1000	20666	NM_009234
Sox14	SRY-box containing gene 14	73636036	20669	XM_284529.3
Sox2	SRY-box containing gene 2	77280331	20674	NM_011443.2
Sox5	SRY-box containing gene 5	1284	20678	NM_011444
Sox8	SRY-box containing gene 8	74988736	20681	NM_011447.1
Sox9	SRY-box containing gene 9	1422	20682	NM_011448
Sp3	trans-acting transcription factor 3	1856	20687	NM_011450
Sp8	trans-acting transcription factor 8	74272904	320145	NM_177082.3
Spag16	sperm associated antigen 16	75080199	66722	NM_029160.1
Spag5	sperm associated antigen 5	72081516	54141	NM_017407.1
Sparc	secreted acidic cysteine rich glycoprotein	73788453	20692	NM_009242.1
Sparc	secreted acidic cysteine rich glycoprotein	73788443	20692	NM_009242.1
Sparcl1	SPARC-like 1 (mast9, hevin)	74750016	13602	NM_010097.2
Spata13	spermatogenesis associated 13	73997152	219140	XM_147847.5
Spdef	SAM pointed domain containing ets transcription factor	2627	30051	NM_013891
Spg21	spastic paraplegia 21 homolog (human)	71717143	27965	NM_138584.1
Spint1	serine protease inhibitor, Kunitz type 1	70813908	20732	NM_016907.2
Spint2	serine protease inhibitor, Kunitz type 2	74047774	20733	NM_011464.1
Spock1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1	72340122	20745	NM_009262.2
Spock3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 3	70634298	72902	NM_023689.2
Spon1	spondin 1, (f-spondin) extracellular matrix protein	71836797	233744	NM_145584.1
Spp1	secreted phosphoprotein 1	70436740	20750	NM_009263.1
Sprn	shadow of prion protein	73512367	212518	NM_183147.1
Sprr1a	small proline-rich protein 1A	1534	20753	NM_009264
Spsb1	splA/ryanodine receptor domain and SOCS box containing 1	77332092	74646	NM_029035.2
Spsb4	splA/ryanodine receptor domain and SOCS box containing 4	75773701	211949	NM_145134.2
Sptlc2	serine palmitoyltransferase, long chain base subunit 2	74658175	20773	NM_011479.2
Sqle	squalene epoxidase	70231996	20775	NM_009270.2
Sqrdl	sulfide quinone reductase-like (yeast)	74047907	59010	NM_021507.4
Srgap1	SLIT-ROBO Rho GTPase activating protein 1	74047745	117600	XM_125904.3
Srgap2	SLIT-ROBO Rho GTPase activating protein 2	316	14270	NM_080448
Srm	spermidine synthase	75041563	20810	TC1568695.1
Srp14	signal recognition particle 14	74750021	20813	NM_009273.2
Srp54	signal recognition particle 54a	2629	24067	NM_011899
Srpr	signal recognition particle receptor ('docking protein')	1593	67398	NM_026130
Srprb	signal recognition particle receptor, B subunit	1536	20818	NM_009275

Ssb	Sjogren syndrome antigen B	75081397	20823	NM_009278.1
Ssbp2	single-stranded DNA binding protein 2	70928385	66970	NM_024186.1
Ssbp4	single stranded DNA binding protein 4	73817987	76900	NM_133772.1
Ssr1	signal sequence receptor, alpha	2631	107513	NM_025965
Ssr2	signal sequence receptor, beta	121097	66256	NM_025448.2
Ssr2	signal sequence receptor, beta	77869814	66256	NM_025448.2
Ssrp1	structure specific recognition protein 1	74819346	20833	NM_182990.1
Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	2633	56390	NM_020491
Sst	somatostatin	1001	20604	NM_009215
Sstr2	somatostatin receptor 2	77371821	20606	NM_009217.1
Sstr4	somatostatin receptor 4	73636037	20608	NM_009219.2
Ssx2ip	synovial sarcoma, X breakpoint 2 interacting protein	73817985	99167	NM_138744.1
St18	suppression of tumorigenicity 18	75038443	240690	NM_173868.1
St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	73616023	20442	NM_009177.2
St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	73732154	54613	NM_018784.1
St6gal1	beta galactoside alpha 2,6 sialyltransferase 1	74658241	20440	NM_145933.2
St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	75077242	20447	NM_011372.1
St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	73787946	26938	NM_012028.2
St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	73787947	26938	NM_012028.2
St6galnac6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	74047902	50935	NM_016973.1
St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	73907494	20449	NM_011374.1
St8sia2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	77925023	20450	NM_009181.1
St8sia3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	73929595	20451	NM_009182.2
St8sia5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	72081445	225742	NM_153124.1
st8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	73929596	241230	NM_145838.1
Stac	src homology three (SH3) and cysteine rich domain	73788116	20840	NM_016853.1
Stac	src homology three (SH3) and cysteine rich domain	73788126	20840	NM_016853.1
Stac2	SH3 and cysteine rich domain 2	293472	217154	NM_146028.2
Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	73931415	20844	NM_011484.2
Stard13	serologically defined colon cancer antigen 13	71587846	243362	NM_146258.1
Stard5	StAR-related lipid transfer (START) domain containing 5	70813909	170460	NM_023377.4
Stard7	START domain containing 7	74800953	99138	NM_139308.1
Stard8	START domain containing 8	73521808	236920	NM_199018.1
Stat1	signal transducer and activator of transcription 1	2635	20846	NM_009283
Stat2	signal transducer and activator of transcription 2	74425571	20847	NM_019963.1
Stat3	signal transducer and activator of transcription 3	2637	20848	NM_011486
Stat5a	signal transducer and activator of transcription 5A	121092	20850	NM_011488.2
Stat5a	signal transducer and activator of transcription 5A	77413690	20850	NM_011488.2
Stat5b	signal transducer and activator of transcription 5B	71016584	20851	NM_011489.2
Stc1	stanniocalcin 1	2639	20855	NM_009285
Stc2	stanniocalcin 2	2641	20856	NM_011491
Steap2	six transmembrane epithelial antigen of prostate 2	71670697	74051	XM_284053.3
Steap3	STEAP family member 3	74881275	68428	NM_133186.1
Stim2	stromal interaction molecule 2	73929869	116873	XM_132038.4
Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	61000	98267	NM_133810.2
Stk24	serine/threonine kinase 24 (STE20 homolog, yeast)	73635773	223255	NM_145465.1
Stk32a	serine/threonine kinase 32A	71920510	269019	NM_178749.2
Stk32c	serine/threonine kinase 32C	70744516	57740	NM_021302.1
Stk33	serine/threonine kinase 33	74641163	117229	XM_358897.2

Stk38l	serine/threonine kinase 38 like	71064288	232533	NM_172734.2
Stk6	aurora kinase A	2643		NM_011497
Stmn1	stathmin 1	71016595	16765	NM_019641.2
Stmn2	stathmin-like 2	74819695	20257	NM_025285.1
Stmn3	stathmin-like 3	1003	20262	NM_009133
Stmn4	stathmin-like 4	1006	56471	NM_019675
Stoml1	stomatin-like 1	74881134	69106	NM_026942.2
Stoml2	stomatin (Epb7.2)-like 2	74581379	66592	NM_023231.2
Stra6	stimulated by retinoic acid gene 6	75041492	20897	NM_009291.1
Strn	striatin, calmodulin binding protein	73521824	268980	NM_011500.1
Stub1	STIP1 homology and U-Box containing protein 1	323389	56424	NM_019719.2
Stx12	syntaxin 12	70928169	100226	NM_133887.2
Stx1a	syntaxin 1A (brain)	2645	20907	NM_016801
Stx3	syntaxin 3	74047924	20908	NM_011502.1
Stxbp1	syntaxin binding protein 1	1009	20910	NM_009295
Stxbp2	syntaxin binding protein 2	75774667	20911	NM_011503.2
Stxbp6	syntaxin binding protein 6 (amisyn)	70744323	217517	NM_144552.1
Suhw3	zinc finger protein 280c	1669	208968	NM_153532
Suhw3	zinc finger protein 280c	77371859	208968	NM_153532.2
Sulf1	sulfatase 1	75041501	240725	NM_172294.1
Sulf2	sulfatase 2	72007935	72043	XM_358343.2
Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	75774114	20887	NM_133670.1
Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	2647	20924	NM_013676
Susd2	sushi domain containing 2	75146000	71733	NM_027890.3
Susd4	sushi domain containing 4	75774678	96935	NM_144796.2
Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	1538	64707	NM_022724
Sv2b	synaptic vesicle glycoprotein 2 b	72104171	64176	NM_153579.3
Sv2c	synaptic vesicle glycoprotein 2c	74357583	75209	XM_127490.3
Svil	supervillin	77332748	225115	NM_153153.1
Syap1	synapse associated protein 1	1858	67043	NM_025932
Syn1	synapsin I	227540	20964	NM_013680.1
Syn2	synapsin II	73929870	20965	NM_013681.1
Syn3	synapsin III	73930808	27204	NM_013722.1
Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	1391	56403	NM_019666
Syne1	synaptic nuclear envelope 1	74640879	64009	NM_153399.1
Syne2	synaptic nuclear envelope 2	74640880	319565	XM_619002.1
Syngr3	synaptogyrin 3	1860	20974	NM_011522
Synj1	synaptojanin 1	1287	104015	XM_358889
Synj2	synaptojanin 2	71064267	20975	NM_011523.1
Synj2bp	synaptojanin 2 binding protein	293040	24071	NM_025292.2
Synj2bp	synaptojanin 2 binding protein	77414884	24071	NM_025292.2
Synpo	synaptopodin	74640881	104027	XM_619543.1
Synpr	synaptoporin	1862	72003	NM_028052
Sypl	synaptophysin-like protein	75233089	19027	NM_013635.2
Syt1	synaptotagmin I	1014	20979	NM_009306
Syt10	synaptotagmin X	1573	54526	NM_018803
Syt10	synaptotagmin X	1017	54526	NM_018803
Syt11	synaptotagmin XI	2649	229521	NM_018804
Syt12	synaptotagmin XII	1291	171180	NM_134164

Syt13	synaptotagmin XIII	1864	80976	NM_030725
Syt13	synaptotagmin XIII	1020	80976	NM_030725
Syt16	synaptotagmin XVI	71358663	238266	NM_172804.1
Syt17	synaptotagmin XVII	73616035	110058	NM_138649.1
Syt2	synaptotagmin II	1023	20980	NM_009307
Syt3	synaptotagmin III	1026	20981	NM_016663
Syt4	synaptotagmin IV	2651	20983	NM_009308
Syt5	synaptotagmin V	1029	53420	NM_016908
Syt6	synaptotagmin VI	1032	54524	NM_018800
Syt7	synaptotagmin VII	1035	54525	NM_018801
Syt9	synaptotagmin IX	73817439	60510	NM_021889.2
Syt12	synaptotagmin-like 2	73520979	83671	NM_031394.1
Syt13	synaptotagmin-like 3	2653	83672	NM_031395
Syt14	synaptotagmin-like 4	75651223	27359	NM_013757.1
Syt15	synaptotagmin-like 5	73930809	236643	NM_177704.2
Tac1	tachykinin 1	1038	21333	NM_009311
Tac2	tachykinin 2	72339556	21334	NM_009312.1
Tac2	tachykinin 2	77279001	21334	NM_009312.1
Tacc3	transforming, acidic coiled-coil containing protein 3	75651179	21335	NM_011524.1
Tacc3	transforming, acidic coiled-coil containing protein 3	70928396	21335	NM_011524.1
Tacr1	tachykinin receptor 1	1295	21336	NM_009313
Tacr3	tachykinin receptor 3	1297	21338	NM_021382
Taf13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor	2655	99730	NM_025444
Tagln3	transgelin 3	75988633	56370	NM_019754.2
Tal1	T-cell acute lymphocytic leukemia 1	72080006	21349	NM_011527.1
Taldo1	transaldolase 1	74988562	21351	NM_011528.1
Taok1	TAO kinase 1	74819235	216965	XM_484053.1
Tas2r144	taste receptor, type 2, member 144	71670733	387515	NM_001001453.1
Tat	tyrosine aminotransferase	2657	234724	NM_146214
Tbc1d1	TBC1 domain family, member 1	71670698	57915	NM_019636.1
Tbc1d14	TBC1 domain family, member 14	71020391	100855	NM_133910.2
Tbc1d8	TBC1 domain family, member 8	71836747	54610	NM_018775.1
Tbl2	transducin (beta)-like 2	1868	27368	NM_013763
Tbl3	transducin (beta)-like 3	248328	213773	NM_145396.3
Tbl3	transducin (beta)-like 3	77413694	213773	NM_145396.3
Tbp	TATA box binding protein	67850950	21374	NM_013684.1
Tbr1	T-box brain gene 1	1041	21375	NM_009322
TC1410973		73512191		
TC1412430		73615573		
TC1412826		73512192		
TC1413297		72109379		
TC1416279		73512193		
TC1460681		72109389		
TC1461568		73512194		
TC1463368		74750065		
TC1463663		71717629		
TC1480430		71717630		
TC1481270		72109399		
TC1515400		75080620		

TC1515580		75080632		
TC1517156		73512195		
TC1517215		73512196		
TC1517671		72109410		
TC1519670		72109423		
TC1536859		73615782		
TC1541413		74641209		
TC1550494		73512197		
TC1551031		73512198		
TC1552471		75080633		
TC1552579		73512199		
TC1556600		73512200		
TC1557025		72109445		
TC1557245		72109467		
TC1559728		72109489		
TC1561123		73512201		
TC1563253		73512202		
TC1563370		74750075		
TC1563468		73512203		
TC1563688		73512204		
TC1564884		73512205		
TC1565734		72109633		
TC1567150		73512206		
TC1568100		71717640		
TC1568600		74988768		
TC1569611	furry homolog-like (Drosophila)	73512207	72313	TC1569611.1
TC1570991		73512208		
Tcea1	transcription elongation factor A (SII) 1	227534	21399	NM_011541.3
Tcea2	transcription elongation factor A (SII), 2	74988737	21400	NM_009326.1
Tcea3	transcription elongation factor A (SII), 3	1870	21401	NM_011542
Tceb3	transcription elongation factor B (SIII), polypeptide 3	75043141	27224	NM_013736.2
Tcerg1	transcription elongation regulator 1 (CA150)	1872	56070	NM_019512
Tcerg1l	transcription elongation regulator 1-like	75041511	70571	NM_183289.1
Tcf19	transcription factor 19	2659	106795	NM_025674
Tcf2	HNF1 homeobox B	1874	21410	NM_009330
Tcf3	transcription factor 3	1424	21415	NM_009332
Tcf4	transcription factor 4	1044	21413	NM_013685
Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	72339557	21416	NM_009333.2
Tcfap2a	transcription factor AP-2, alpha	2661	21418	NM_011547
Tcfap2c	transcription factor AP-2, gamma	74047843	21420	NM_009335.1
Tcfe2a	transcription factor E2a	67850951	21423	NM_011548.3
Tcfl4	MAX-like protein X	227539	21428	NM_011550.2
Tcn2	transcobalamin 2	71924389	21452	NM_015749.1
Tcte1l	dynein light chain Tctex-type 3	74425518	67117	NM_025975.3
Tde2	serine incorporator 1	67752306	56442	NM_019760.1
Tdg	thymine DNA glycosylase	71020392	21665	NM_011561.1
Tdo2	tryptophan 2,3-dioxygenase	71717618	56720	NM_019911.2
Tdrd3	tudor domain containing 3	73817944	219249	NM_172605.2
Tdrd3	tudor domain containing 3	77887882	219249	NM_172605.2

Tecta	tectorin alpha	74882940	21683	NM_009347.1
Tegt	testis enhanced gene transcript	2663	110213	NM_026669
Tekt1	tektin 1	75080238	21689	NM_011569.1
Tera	teratocarcinoma expressed, serine rich	75081207	56306	NM_019643.1
Tera	teratocarcinoma expressed, serine rich	1878	56306	NM_019643
Terf2ip	telomeric repeat binding factor 2, interacting protein	2665	57321	NM_020584
Tesc	tescalcin	70634149	57816	NM_021344.2
Tesp1	testicular serine protease 1	74749944	21755	NM_009355.1
Tex261	testis expressed gene 261	74047919	21766	NM_009357.1
Tex27	zinc finger, AN1-type domain 3	293694	21769	NM_148926.1
Tex292	cirrrosis, autosomal recessive 1A (human)	322960	21771	NM_011574.1
Tfam	transcription factor A, mitochondrial	67936016	21780	NM_009360.2
Tff1	trefoil factor 1	1049	21784	NM_009362
Tff1	trefoil factor 1	2679	21784	NM_009362
Tgfb1	transforming growth factor, beta 1	130914	21803	NM_011577.1
Tgfb1i4	TSC22 domain family, member 1	1051		NM_009366
Tgfb2	transforming growth factor, beta 2	70927304	21808	NM_009367.1
Tgfb2	transforming growth factor, beta 2	77869842	21808	NM_009367.1
Tgfb3	transforming growth factor, beta 3	2667	21809	NM_009368
Tgfb2	transforming growth factor, beta receptor II	74819696	21813	NM_009371.2
Tgif	TG interacting factor 1	67850949	21815	NM_009372.2
Th	tyrosine hydroxylase	1056	21823	NM_009377
Thap1	THAP domain containing, apoptosis associated protein 1	44	73754	NM_199042
Thbd	thrombomodulin	75079800	21824	NM_009378.1
Thbs2	thrombospondin 2	73929578	21826	NM_011581.1
Thbs3	thrombospondin 3	74657923	21827	NM_013691.1
Thbs4	thrombospondin 4	71670699	21828	NM_011582.1
Thbs4	thrombospondin 4	77874596	21828	NM_011582.1
Them2	thioesterase superfamily member 2	75042252	66834	NM_025790.1
Thnsl1	threonine synthase-like 1 (bacterial)	74988343	208967	NM_001001297.1
Thpo	thrombopoietin	2671	21832	NM_009379
Thra	thyroid hormone receptor alpha	2673	21833	NM_178060
Thrap4	mediator complex subunit 24	2675	23989	NM_011869
Thrap6	mediator complex subunit 30	248329	69790	NM_027212.1
Thrb	thyroid hormone receptor beta	71249069	21834	NM_009380.1
Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	71587845	21835	NM_009381.2
Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	77874606	21835	NM_009381.2
Thsd6	ADAMTS-like 5	71063847	66548	NM_025629.1
Tiam1	T-cell lymphoma invasion and metastasis 1	72283789	21844	NM_009384.1
Tiam1	T-cell lymphoma invasion and metastasis 1	1059	21844	NM_009384
Tiam2	T-cell lymphoma invasion and metastasis 2	75041513	24001	NM_011878.1
Ticam1	toll-like receptor adaptor molecule 1	72081545	106759	NM_174989.1
Tieg1	Kruppel-like factor 10	70744519	21847	NM_013692.1
Timm13a	translocase of inner mitochondrial membrane 10 homolog (yeast)	73521825	30059	NM_013899.1
Timp2	tissue inhibitor of metalloproteinase 2	75988524	21858	NM_011594.2
Timp3	tissue inhibitor of metalloproteinase 3	73769324	21859	NM_011595.1
Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	293470	28113	NM_145705.2
Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	77414587	28113	NM_145705.2
Titf1	NK2 homeobox 1	74988460	21869	NM_009385.2

Tk2	thymidine kinase 2, mitochondrial	75042260	57813	NM_021028.2
Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	1061	21885	NM_011599
Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	2681	21887	NM_009389
Tle4	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	73521809	21888	NM_011600.2
Tll1	tolloid-like	74272905	21892	NM_009390.1
Tm2d3	TM2 domain containing 3	83167	68634	NM_026795.1
Tm2d3	TM2 domain containing 3	77414123	68634	NM_026795.1
Tm4sf1	transmembrane 4 superfamily member 1	74882950	17112	NM_008536.2
Tm4sf11	plasma membrane proteolipid	1880		NM_026385
Tm6sf1	transmembrane 6 superfamily member 1	71836883	107769	NM_145375.1
Tm7sf3	transmembrane 7 superfamily member 3	1543	67623	XM_132970
Tm7sf3	transmembrane 7 superfamily member 3	77874614	67623	XM_132970.4
Tmc1	transmembrane channel-like gene family 1	75041514	13409	NM_028953.1
Tmc6	transmembrane channel-like gene family 6	70928250	217353	NM_145439.1
Tmc6	transmembrane channel-like gene family 6	77887880	217353	NM_145439.1
Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	1299	230157	NM_021436
Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	77395095	230157	NM_021436.1
Tmeff2	transmembrane protein with EGF-like and two follistatin-like domains 2	71015807	56363	NM_019790.2
Tmem1	transmembrane protein 1	1063	216131	XM_125775
Tmem11	transmembrane protein 11	75043144	216821	NM_173453.1
Tmem126a	transmembrane protein 126A	77414913	66271	NM_025460.1
Tmem14a	transmembrane protein 14A	323591	75712	NM_029398.1
Tmem14a	transmembrane protein 14A	77414600	75712	NM_029398.1
Tmem16b	transmembrane protein 16B	71587834	243634	NM_153589.1
Tmem16f	transmembrane protein 16F	71924067	105722	NM_175344.3
Tmem16f	transmembrane protein 16F	77887878	105722	NM_175344.3
Tmem2	transmembrane protein 2	1409	83921	
Tmem24	transmembrane protein 24	73592532	71764	XM_134795.3
Tmem25	transmembrane protein 25	71670700	71687	NM_027865.1
Tmem32	transmembrane protein 32	276068	236792	NM_146234.2
Tmem32	transmembrane protein 32	77414585	236792	NM_146234.2
Tmem33	transmembrane protein 33	356284	67878	NM_028975.2
Tmem33	transmembrane protein 33	77887844	67878	NM_028975.2
Tmem46	transmembrane protein 46	75043156	219134	NM_145463.3
Tmem47	transmembrane protein 47	75081394	192216	NM_138751.1
Tmem63c	transmembrane protein 63c	76115724	217733	NM_172583.2
Tmem64	transmembrane protein 64	322957	100201	NM_181401.2
Tmem64	transmembrane protein 64	77414589	100201	NM_181401.2
Tmie	transmembrane inner ear	74957868	20776	NM_146260.1
Tmod1	tropomodulin 1	75988526	21916	NM_021883.1
Tmprss5	transmembrane protease, serine 5 (spinesin)	74957887	80893	NM_030709.1
Tmsb10	thymosin, beta 10	73521810	19240	NM_025284.2
Tnc	tenascin C	71717115	21923	NM_011607.1
Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	2685	21927	NM_009395
Tnfaip3	tumor necrosis factor, alpha-induced protein 3	75084101	21929	NM_009397.2
Tnfaip8	tumor necrosis factor, alpha-induced protein 8	75038412	106869	NM_134131.1
Tnfaip8l3	tumor necrosis factor, alpha-induced protein 8-like 3	76097700	244882	XM_146997.2
Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a	199393	21934	NM_009399.2
Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	2687	27279	NM_013749



Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	74425524	29820	NM_013869.3
Tnfrsf19l	RELT tumor necrosis factor receptor	77869869	320100	NM_177073.3
Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	2689	21937	NM_011609
Tnfrsf21	tumor necrosis factor receptor superfamily, member 21	71836885	94185	NM_178589.2
Tnfrsf25	tumor necrosis factor receptor superfamily, member 25	121096	85030	NM_033042.2
Tnfrsf25	tumor necrosis factor receptor superfamily, member 25	77925097	85030	NM_033042.2
Tnip2	TNFAIP3 interacting protein 2	74425540	231130	NM_139064.1
Tnmd	tenomodulin	71924343	64103	NM_022322.2
Tnnc1	troponin C, cardiac/slow skeletal	73817440	21924	NM_009393.1
Tnni1	troponin I, skeletal, slow 1	75774109	21952	NM_021467.4
Tnni3	troponin I, cardiac	1065	21954	NM_009406
Tnnt1	troponin T1, skeletal, slow	77280576	21955	NM_011618.1
Tnnt3	troponin T3, skeletal, fast	61411	21957	NM_011620.1
Tnr	tenascin R	73930819	21960	NM_022312.1
Tnrc4	trinucleotide repeat containing 4	74641324	78784	NM_172434.1
Tnrc6		314		XM_486002
Tnrc9	TOX high mobility group box family member 3	75077172	244579	NM_172913.1
Tns3	tensin 3	75080694	319939	XM_109868
Tnxb	tenascin XB	74749957	81877	NM_031176.1
Tob2	transducer of ERBB2, 2	77340500	57259	NM_020507.2
Tom1l2	target of myb1-like 2 (chicken)	74749970	216810	NM_153080.1
Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)	74819230	67952	NM_024214.1
Tomm34	translocase of outer mitochondrial membrane 34	75042253	67145	NM_025996.1
Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	320	28185	NM_138599
Top1	topoisomerase (DNA) I	74957897	21969	NM_009408.1
Top2a	topoisomerase (DNA) II alpha	1301	21973	NM_011623
Tox	thymocyte selection-associated HMG box gene	71670691	252838	NM_145711.2
Tpbg	trophoblast glycoprotein	76085743	21983	NM_011627.2
Tpd52l1	tumor protein D52-like 1	74357570	21987	NM_009413.1
Tph2	tryptophan hydroxylase 2	74511925	216343	NM_173391.1
Tpm3	tropomyosin 3, gamma	275873	59069	NM_022314.2
Tpr	translocated promoter region	72104172	108989	NM_133780.2
Tra1	heat shock protein 90kDa beta (Grp94), member 1	75042251	22027	NM_011631.1
Traf2	Tnf receptor-associated factor 2	2691	22030	NM_009422
Traf5	Tnf receptor-associated factor 5	2693	22033	NM_011633
Traf7	Tnf receptor-associated factor 7	2527	224619	NM_153792
Traip	TRAF-interacting protein	199396	22036	NM_011634.2
Traip	TRAF-interacting protein	77887842	22036	NM_011634.2
Trap1	TNF receptor-associated protein 1	1966	68015	NM_026508
Trappc1	trafficking protein particle complex 1	71670701	245828	XM_126252.4
Trar3		71587941	215861	XM_137001.3
Trem2	triggering receptor expressed on myeloid cells 2	67870433	83433	NM_031254.2
Trerf1	transcriptional regulating factor 1	75651165	224829	NM_172622.1
Trh	thyrotropin releasing hormone	71016631	22044	NM_009426.1
Trhde	TRH-degrading enzyme	544707	237553	NM_146241.1
Trhde	TRH-degrading enzyme	75774669	237553	NM_146241.1
Trhr	thyrotropin releasing hormone receptor	72008492	22045	NM_013696.1
Trhr	thyrotropin releasing hormone receptor	1303	22045	NM_013696
Trib1	tribbles homolog 1 (Drosophila)	71015818	211770	NM_144549.2

Trib2	tribbles homolog 2 (Drosophila)	71587811	217410	NM_144551.3
Trim16	tripartite motif protein 16	73931416	94092	NM_053169.1
Trim23	tripartite motif protein 23	74749983	81003	NM_030731.1
Trim25	tripartite motif protein 25	1545	217069	NM_009546
Trim28	tripartite motif protein 28	1071	21849	NM_011588
Trim3	tripartite motif protein 3	73732147	55992	NM_018880.1
Trim36	tripartite motif-containing 36	74657930	28105	NM_178872.3
Trim37	tripartite motif protein 37	74749996	68729	NM_197987.1
Trim9	tripartite motif protein 9	1074	94090	NM_053167
Trip10	thyroid hormone receptor interactor 10	2696	106628	NM_134125
Trip4	thyroid hormone receptor interactor 4	1924	56404	NM_019797
Tro	trophinin	74819332	56191	NM_001002272.1
Trp53	transformation related protein 53	67855414	22059	NM_011640.1
Trp53bp1	transformation related protein 53 binding protein 1	71836834	27223	NM_013735.2
Trp53i11	transformation related protein 53 inducible protein 11	73521826	277414	XM_203859.4
Trp73	transformation related protein 73	73929579	22062	NM_011642.1
Trpc2	transient receptor potential cation channel, subfamily C, member 2	73592539	22064	NM_011644.1
Trpc4	transient receptor potential cation channel, subfamily C, member 4	1305	22066	NM_016984
Trpc5	transient receptor potential cation channel, subfamily C, member 5	71247658	22067	NM_009428.1
Trpc6	transient receptor potential cation channel, subfamily C, member 6	70562126	22068	NM_013838.1
Trpm1	transient receptor potential cation channel, subfamily M, member 1	75081002	17364	XM_358370.2
Trpm6	transient receptor potential cation channel, subfamily M, member 6	73907502	225997	NM_153417.1
Trps1	trichorhinophalangeal syndrome I (human)	2697	83925	NM_032000
Trpv4	transient receptor potential cation channel, subfamily V, member 4	73992707	63873	NM_022017.1
Tsc2	tuberous sclerosis 2	1431	22084	NM_011647
Tsc22d2	TSC22 domain family 2	74958463	72033	XM_485240.1
Tsc22d3	TSC22 domain family 3	74581366	14605	NM_010286.2
Tsfm	Ts translation elongation factor, mitochondrial	72129246	66399	NM_025537.2
Tsg101	tumor susceptibility gene 101	74047878	22088	NM_021884.1
Tsga2	radial spoke head 1 homolog (Chlamydomonas)	1077	22092	NM_025290
Tslpr	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	1882		NM_016715
Tspan12	tetraspanin 12	73997153	269831	NM_173007.1
Tspan18	tetraspanin 18	74357573	241556	NM_183180.1
Tspan2	tetraspanin 2	75144618	70747	NM_027533.1
Tspan32	tetraspanin 32	72129242	27027	NM_020286.2
Tspan5	tetraspanin 5	74657928	56224	NM_019571.1
Tspan6	tetraspanin 6	74047839	56496	NM_019656.2
Tspyl2	TSPY-like 2	73817931	52808	NM_029836.1
Ttbk1	tau tubulin kinase 1	75147759	140810	NM_001024856.1
Ttc3	tetratricopeptide repeat domain 3	1079	22129	NM_009441
Ttl4	tubulin tyrosine ligase-like family, member 4	71670702	67534	XM_129771.6
Ttn	titin	74047746	22138	XM_130322.4
Ttyh3	tweety homolog 3 (Drosophila)	74988711	78339	NM_175274.2
Tuba4	tubulin, alpha 4A	70616005	22145	NM_009447.2
Tubb2	tubulin, beta 2a	74819689	22151	NM_009450.1
Tubb4	tubulin, beta 4	1081	22153	NM_009451
Tulp4	tubby like protein 4	2699	68842	NM_054040
Tusc4	tumor suppressor candidate 4	2701	56032	NM_018879
Txn2	thioredoxin 2	71670705	56551	NM_019913.3

Txnip	thioredoxin interacting protein	1084	56338	NM_023719
Txnrd1	thioredoxin reductase 1	74988746	50493	NM_015762.1
Txnrd3	thioredoxin reductase 3	71670706	232223	NM_153162.2
Tyr	tyrosinase	2703	22173	NM_011661
Tyro3	TYRO3 protein tyrosine kinase 3	72119607	22174	NM_019392.1
Uaca	uveal autoantigen with coiled-coil domains and ankyrin repeats	74800883	72565	NM_028283.1
Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	70743895	107652	NM_133806.2
Ubap1	ubiquitin-associated protein 1	74957898	67123	NM_023305.2
Ubash3a	ubiquitin associated and SH3 domain containing, A	1086	328795	NM_177823
Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	74750009	22210	NM_009458.2
Ube2e3	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	75651166	22193	NM_009454.2
Ube2g2	ubiquitin-conjugating enzyme E2G 2	1547	22213	NM_019803
Ube2h	ubiquitin-conjugating enzyme E2H	74583203	22214	NM_009459.2
Ube2i	ubiquitin-conjugating enzyme E2I	45666	22196	NM_011665.2
Ube3a	ubiquitin protein ligase E3A	1926	22215	NM_011668
Ube3c	ubiquitin protein ligase E3C	71670707	100763	NM_133907.1
Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	74750010	63958	NM_022022.1
Ubl3	ubiquitin-like 3	1884	24109	NM_011908
Ubl4	ubiquitin-like 4	75774670	27643	NM_145405.1
Ubr1	ubiquitin protein ligase E3 component n-recognin 1	74957908	22222	NM_009461.1
Ubtf	upstream binding transcription factor, RNA polymerase I	74988738	21429	NM_011551.2
Uchl1	ubiquitin carboxy-terminal hydrolase L1	1088	22223	NM_011670
Uck1	uridine-cytidine kinase 1	293666	22245	NM_011675.1
Ucn	urocortin	1435	22226	NM_021290
Ucn3	urocortin 3	1091	83428	NM_031250
Ufm1	ubiquitin-fold modifier 1	72129283	67890	NM_026435.2
Ugalt2	solute carrier family 35, member B1	70928159	110172	NM_016752.1
Ugcgl1	UDP-glucose ceramide glucosyltransferase-like 1	74957909	320011	NM_198899.1
Ugdh	UDP-glucose dehydrogenase	77280339	22235	NM_009466.2
Ugp2	UDP-glucose pyrophosphorylase 2	2705	216558	NM_139297
Ugt8	UDP galactosyltransferase 8A	655116	22239	NM_011674.2
Unc13c	unc-13 homolog C (C. elegans)	2707	208898	XM_146948
Unc5b	unc-5 homolog B (C. elegans)	74274687	107449	NM_029770.1
Unc5c	unc-5 homolog C (C. elegans)	71670708	22253	NM_009472.1
Unc5d	unc-5 homolog D (C. elegans)	71924239	210801	NM_153135.1
Unc84a	unc-84 homolog A (C. elegans)	74425548	77053	NM_024451.1
Unc84b	unc-84 homolog B (C. elegans)	74658032	223697	NM_194342.1
Uncx4.1	Unc4.1 homeobox (C. elegans)	1438	22255	NM_013702
Upp1	uridine phosphorylase 1	71836877	22271	NM_009477.1
Uqcr	ubiquinol-cytochrome c reductase (6.4kD) subunit	67870133	66594	NM_025650.1
Uqcrb	ubiquinol-cytochrome c reductase binding protein	323595	67530	NM_026219.1
Uqcrc2	ubiquinol cytochrome c reductase core protein 2	655502	67003	NM_025899.1
Uqcrcf1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	71924399	66694	NM_025710.1
Uqcrrh	ubiquinol-cytochrome c reductase hinge protein	77340502	66576	NM_025641.2
Usmg5	upregulated during skeletal muscle growth 5	67862431	66477	NM_023211.1
Usp11	ubiquitin specific peptidase 11	355883	236733	NM_145628.2
Usp11	ubiquitin specific peptidase 11	77869130	236733	NM_145628.2
Usp13	ubiquitin specific peptidase 13 (isopeptidase T-3)	74957910	72607	XM_130826.4
Usp14	ubiquitin specific peptidase 14	74881157	59025	NM_021522.2

Usp16	ubiquitin specific peptidase 16	1886	74112	NM_024258
Usp20	ubiquitin specific peptidase 20	72104170	74270	NM_028846.2
Usp21	ubiquitin specific peptidase 21	2711	30941	NM_013919
Usp22	ubiquitin specific peptidase 22	74957911	216825	NM_001004143.1
Usp25	ubiquitin specific peptidase 25	2713	30940	NM_013918
Usp31	ubiquitin specific peptidase 31	149	76179	XM_485461
Usp46	ubiquitin specific peptidase 46	70805955	69727	NM_177561.2
Ust	uronyl-2-sulfotransferase	71670734	338362	NM_177387.2
Utp14b	UTP14, U3 small nucleolar ribonucleoprotein, homolog B (yeast)	71924249	195434	NM_001001981.1
Utrn	utrophin	73929872	22288	NM_011682.3
Uts2d	urotensin 2 domain containing	75144621	224065	NM_198166.2
Vamp1	vesicle-associated membrane protein 1	75651233	22317	NM_009496.2
Vamp2	vesicle-associated membrane protein 2	1092	22318	NM_009497
Vangl1	vang-like 1 (van gogh, Drosophila)	71670709	229658	NM_177545.2
Vat1	vesicle amine transport protein 1 homolog (T californica)	74357572	26949	NM_012037.1
Vav2	vav 2 oncogene	74583149	22325	NM_009500.1
Vav3	vav 3 oncogene	76085746	57257	NM_020505.1
Vcam1	vascular cell adhesion molecule 1	323390	22329	NM_011693.2
Vcam1	vascular cell adhesion molecule 1	77414897	22329	NM_011693.2
Vdac1	voltage-dependent anion channel 1	74957912	22333	NM_011694.1
Vdac2	voltage-dependent anion channel 2	1888	22334	NM_011695
Vdac3	voltage-dependent anion channel 3	1549	22335	NM_011696
Vdr	vitamin D receptor	1928	22337	NM_009504
Vegfa	vascular endothelial growth factor A	74988747	22339	NM_009505.2
Vegfb	vascular endothelial growth factor B	75079746	22340	NM_011697.1
Veph1	ventricular zone expressed PH domain homolog 1 (zebrafish)	74988352	72789	NM_028357.1
Viaat	solute carrier family 32 (GABA vesicular transporter), member 1	1098		NM_009508
Vil1	villin 1	1440	22349	NM_009509
Vil2	villin 2	2715	22350	NM_009510
Vill	villin-like	71015194	22351	NM_011700.1
Vim	vimentin	1309	22352	NM_011701
Vip	vasoactive intestinal polypeptide	77371835	22353	NM_011702.1
Vipr2	vasoactive intestinal peptide receptor 2	1104	22355	NM_009511
Vldlr	very low density lipoprotein receptor	121089	22359	NM_013703.1
Vldlr	very low density lipoprotein receptor	77413688	22359	NM_013703.1
Vmd2l1	bestrophin 2	1930	212989	NM_145388
Vmp	neurensin 1	71358557	22360	NM_009513.1
Vps18	vacuolar protein sorting 18 (yeast)	1325	228545	NM_172269
Vps35	vacuolar protein sorting 35	355884	65114	NM_022997.2
Vps35	vacuolar protein sorting 35	77869144	65114	NM_022997.2
Vps39	vacuolar protein sorting 39 (yeast)	74047842	269338	NM_147153.2
Vsnl1	visinin-like 1	1106	26950	NM_012038
Vtn	vitronectin	67752116	22370	NM_011707.1
Vwa1	von Willebrand factor A domain containing 1	72007936	246228	NM_147776.2
Vwc2	von Willebrand factor C domain containing 2	77332096		NM_177033.2
Vwcd1	cache domain containing 1	72119579	320508	NM_198037.1
Wbp5	WW domain binding protein 5	71717602	22381	NM_011712.1
Wbscr14	MLX interacting protein-like	1932		NM_021455
Wbscr17	Williams-Beuren syndrome chromosome region 17 homolog (human)	1934	212996	NM_145218

Wbscr21	abhydrolase domain containing 11	1577		NM_145215
Wdr18	WD repeat domain 18	1551	216156	NM_175450
Wdr21	WD repeat domain 21	2717	73828	NM_030246
Wdr31	WD repeat domain 31	2719	71354	NM_023597
Wdr47	WD repeat domain 47	74819248	99512	NM_181400.2
Wdr5	WD repeat domain 5	227159	140858	NM_080848.1
Wdr8	WD repeat domain 8	75042258	59002	NM_021499.1
Wdr9	bromodomain and WD repeat domain containing 1	1109		NM_145125
Wfs1	Wolfram syndrome 1 homolog (human)	74881161	22393	NM_011716.1
Whrn	whirlin	77371813	73750	NM_001008791.1
Wif1	Wnt inhibitory factor 1	74511885	24117	NM_011915.1
Wif1	Wnt inhibitory factor 1	1111	24117	NM_011915
Wnt1	wingless-related MMTV integration site 1	2721	22408	NM_021279
Wnt10a	wingless related MMTV integration site 10a	2723	22409	NM_009518
Wnt10b	wingless related MMTV integration site 10b	2725	22410	NM_011718
Wnt11	wingless-related MMTV integration site 11	2727	22411	NM_009519
Wnt2b	wingless related MMTV integration site 2b	1589	22414	NM_009520
Wnt3	wingless-related MMTV integration site 3	2731	22415	NM_009521
Wnt4	wingless-related MMTV integration site 4	1444	22417	NM_009523
Wnt5a	wingless-related MMTV integration site 5A	67936007	22418	NM_009524.2
Wnt5a	wingless-related MMTV integration site 5A	2733	22418	NM_009524
Wnt6	wingless-related MMTV integration site 6	2735	22420	NM_009526
Wnt7a	wingless-related MMTV integration site 7A	1936	22421	NM_009527
Wnt7b	wingless-related MMTV integration site 7B	72081555	22422	NM_009528.2
Wnt7b	wingless-related MMTV integration site 7B	1113	22422	NM_009528
Wnt8a	wingless-related MMTV integration site 8A	1115	20890	NM_009290
Wnt8b	wingless related MMTV integration site 8b	1890	22423	NM_011720
Wnt9a	wingless-type MMTV integration site 9A	72008493	216795	NM_139298.1
Wnt9b	wingless-type MMTV integration site 9B	1892	22412	NM_011719
Wrb	tryptophan rich basic protein	1117	71446	NM_207301
Wwox	WW domain-containing oxidoreductase	72077451	80707	NM_019573.2
Xbp1	X-box binding protein 1	1119	22433	NM_013842
Xkh	Kell blood group precursor (McLeod phenotype) homolog	71670735	22439	NM_023500.1
Xlkd1	lymphatic vessel endothelial hyaluronan receptor 1	71015813	114332	NM_053247.3
Xlr3a	X-linked lymphocyte-regulated 3A	75650861	22445	NM_011726.1
Yars	tyrosyl-tRNA synthetase	1122	107271	NM_134151
Ybx2	Y box protein 2	75080250	53422	NM_016875.1
Yeats2	YEATS domain containing 2	74988249	208146	XM_148273.5
Yipf1	Yip1 domain family, member 1	74881163	230584	NM_145550.1
Yme111	YME1-like 1 (S. cerevisiae)	356849	27377	NM_013771.2
Ysg2	sialic acid acetyltransferase	324008	22619	NM_011734.2
Ysk4	Yeast Sps1/Stp20-related kinase 4 (S. cerevisiae)	75988578	22625	XM_136210.5
Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	2737	54401	NM_018753
Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	2739	22627	NM_009536
Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	1124	22628	NM_018871
Ywhah	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	1127	22629	NM_011738
Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	1130	22630	NM_011739
Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	1133	22631	NM_011740
Za20d2	zinc finger, AN1-type domain 5	1140	22682	NM_009551

Zbtb16	zinc finger and BTB domain containing 16	71717125	235320	XM_134826.3
Zbtb20	zinc finger and BTB domain containing 20	1143	56490	NM_019778
Zbtb24	zinc finger and BTB domain containing 24	73592542	268294	NM_153398.2
Zcchc12	zinc finger, CCHC domain containing 12	73817424	72693	NM_028325.1
Zcwc3	zinc finger, AN1-type domain 3	1311	21769	XM_128334
Zdhhc2	zinc finger, DHHC domain containing 2	72128751	70546	NM_178395.2
Zdhhc23	zinc finger, DHHC domain containing 23	74363345	332175	NM_001007460.1
Zdhhc7	zinc finger, DHHC domain containing 7	74881264	102193	NM_133967.3
Zdhhc9	zinc finger, DHHC domain containing 9	74425545	208884	NM_172465.1
Zfand2b	zinc finger, AN1 type domain 2B	71836831	68818	NM_026846.1
Zfand3	zinc finger, AN1-type domain 3	77414923		NM_148926.1
Zfhx1b	zinc finger E-box binding homeobox 2	71924066	24136	NM_015753.2
Zfhx4	zinc finger homeodomain 4	74988739	80892	NM_030708.1
Zfp114	zinc finger protein 114	74957922	232966	XM_149897.4
Zfp189	zinc finger protein 189	199388	230162	NM_145547.1
Zfp189	zinc finger protein 189	77414121	230162	NM_145547.1
Zfp191	zinc finger protein 191	1894	59057	NM_021559
Zfp198	zinc finger, MYM-type 2	73925714	76007	NM_029498.2
Zfp238	zinc finger protein 238	2741	30928	NM_013915
Zfp260	zinc finger protein 260	75080996	26466	NM_011981.2
Zfp294	zinc finger protein 294	2747	78913	NM_015565
Zfp312	Fez family zinc finger 2	75651163	54713	NM_080433.1
Zfp330	zinc finger protein 330	75081398	30932	NM_145600.1
Zfp358	zinc finger protein 358	2743	140482	NM_080461
Zfp364	zinc finger protein 364	70743900	67845	NM_026406.2
Zfp365	zinc finger protein 365	73929873	216049	NM_178679.1
Zfp423	zinc finger protein 423	1607	94187	NM_033327
Zfp462	zinc finger protein 462	71670736	242466	NM_172867.1
Zfp521	zinc finger protein 521	71015801	225207	NM_145492.1
Zfp533	zinc finger protein 533	72128752	241494	NM_178723.3
Zfp536	zinc finger protein 536	71836801	243937	NM_172385.1
Zfp537	teashirt zinc finger family member 3	73521811	243931	NM_172298.1
Zfp57	zinc finger protein 57	72103842	22715	NM_009559.2
Zfp61	zinc finger protein 61	75749409	22719	NM_009561.1
Zfpm2	zinc finger protein, multitype 2	71358673	22762	NM_011766.2
Zfpm2	zinc finger protein, multitype 2	75651162	22762	NM_011766.2
Zfpn1a1	IKAROS family zinc finger 1	1144	22778	NM_009578
Zfyve28	zinc finger, FYVE domain containing 28	75934919	231125	XM_132032.4
Zfyve9	zinc finger, FYVE domain containing 9	73521827	230597	XM_131643.5
Zic1	zinc finger protein of the cerebellum 1	72103843	22771	NM_009573.2
Zim1	zinc finger, imprinted 1	71670692	22776	NM_011769.3
Zim2	zinc finger, imprinted 2	76135811	76637	XM_489216.1
Zmynd11	zinc finger, MYND domain containing 11	70743906	66505	NM_144516.1
Znrf1	zinc and ring finger 1	74581382	170737	NM_133206.1
Zswim6	zinc finger, SWIM domain containing 6	75146003	67263	XM_358311.2
Zyx	zyxin	71670710	22793	NM_011777.1

**Supplementary Table 5.** The AGEA dataset including gene symbol, gene name, ABA image ID, Entrez Gene ID and NCBI accession number.

Category	Gene Ontology Term	Count	Percent
GOTERM_BP_5	synaptic transmission	104	2.79%
GOTERM_BP_5	ion transport	277	7.43%
GOTERM_BP_5	neuron differentiation	117	3.14%
	cellular morphogenesis		
GOTERM_BP_5	during differentiation	90	2.41%
	neuron morphogenesis		
GOTERM_BP_5	during differentiation	83	2.23%
GOTERM_BP_5	cell migration	101	2.71%
GOTERM_BP_5	cation transport	173	4.64%
	enzyme linked receptor		
	protein signaling		
GOTERM_BP_5	pathway	97	2.60%
GOTERM_BP_5	axon guidance	42	1.13%
	second-messenger-		
GOTERM_BP_5	mediated signaling	50	1.34%
	Wnt receptor signaling		
GOTERM_BP_5	pathway	49	1.31%
GOTERM_BP_5	anion transport	68	1.82%
GOTERM_BP_5	brain development	48	1.29%
GOTERM_BP_5	phosphate metabolism	220	5.90%
GOTERM_BP_5	regulation of cell size	45	1.21%
GOTERM_BP_5	cell growth	43	1.15%
GOTERM_BP_5	neuron migration	24	0.64%
	regulated secretory		
GOTERM_BP_5	pathway	23	0.62%
	positive regulation of		
	adenylate cyclase		
GOTERM_BP_5	activity	12	0.32%
	neurotransmitter		
GOTERM_BP_5	secretion	21	0.56%
	neurotransmitter		
GOTERM_BP_5	transport	24	0.64%
	regulation of		
GOTERM_BP_5	neurogenesis	20	0.54%
	regulation of		
	progression through		
GOTERM_BP_5	cell cycle	103	2.76%
	neurotransmitter		
GOTERM_BP_5	biosynthesis	10	0.27%
GOTERM_BP_5	amine transport	30	0.80%
GOTERM_BP_5	blood vessel	47	1.26%

	morphogenesis		
	negative regulation of		
	progression through		
GOTERM_BP_5	cell cycle	37	0.99%
0			
GOTERM_BP_5	protein kinase cascade	64	1.72%
	positive regulation of		
GOTERM_BP_5	axonogenesis	9	0.24%
	negative regulation of		
GOTERM_BP_5	signal transduction	29	0.78%
	negative regulation of		
GOTERM_BP_5	cell proliferation	33	0.88%
	amino acid derivative		
GOTERM_BP_5	metabolism	26	0.70%
GOTERM_BP_5	apoptosis	126	3.38%
	amino acid derivative		
GOTERM_BP_5	biosynthesis	13	0.35%
GOTERM_BP_5	regulation of apoptosis	87	2.33%
GOTERM_BP_5	secretory pathway	54	1.45%
GOTERM_BP_5	cation homeostasis	32	0.86%
GOTERM_BP_5	angiogenesis	37	0.99%
GOTERM_BP_5	amino acid transport	23	0.62%
GOTERM_BP_5	sterol metabolism	23	0.62%
	regulation of axon		
GOTERM_BP_5	extension	9	0.24%
	regulation of Wnt		
	receptor signaling		
GOTERM_BP_5	pathway	10	0.27%
	synaptic vesicle		
GOTERM_BP_5	transport	12	0.32%
GOTERM_BP_5	phenol metabolism	11	0.29%
	regulation of		
GOTERM_BP_5	programmed cell death	87	2.33%
GOTERM_BP_5	dopamine metabolism	8	0.21%
	biogenic amine		
GOTERM_BP_5	metabolism	20	0.54%
GOTERM_BP_5	carbohydrate transport	18	0.48%
	vesicle-mediated		
GOTERM_BP_5	transport	88	2.36%
	neuroblast		
GOTERM_BP_5	proliferation	9	0.24%
GOTERM_BP_5	exocytosis	23	0.62%
	cellular carbohydrate		
GOTERM_BP_5	metabolism	72	1.93%
GOTERM_BP_5	negative regulation of	63	1.69%



	cellular metabolism		
	ureteric bud		
GOTERM_BP_5	development	12	0.32%
	carboxylic acid		
GOTERM_BP_5	transport	25	0.67%
GOTERM_BP_5	organic acid transport	25	0.67%
GOTERM_BP_5	steroid metabolism	39	1.05%
	biopolymer		
GOTERM_BP_5	modification	335	8.98%
	cellular lipid		
GOTERM_BP_5	metabolism	108	2.90%
	regulation of MAPKKK		
GOTERM_BP_5	cascade	5	0.13%
GOTERM_BP_5	lung development	15	0.40%
	peptide hormone		
GOTERM_BP_5	processing	6	0.16%
	regulation of		
	progression through		
GOTERM_BP_5	mitotic cell cycle	10	0.27%
GOTERM_BP_5	ossification	24	0.64%
	positive regulation of		
GOTERM_BP_5	cell proliferation	33	0.88%
	skeletal muscle		
GOTERM_BP_5	development	13	0.35%
	metanephros		
GOTERM_BP_5	development	14	0.38%
	substrate-bound cell		
GOTERM_BP_5	migration	5	0.13%
	odontogenesis (sensu		
GOTERM_BP_5	Vertebrata)	10	0.27%
GOTERM_BP_5	neuron maturation	13	0.35%
	regulation of		
	microtubule		
	polymerization or		
GOTERM_BP_5	depolymerization	7	0.19%
	negative regulation of		
	Wnt receptor signaling		
GOTERM_BP_5	pathway	7	0.19%
	negative regulation of		
GOTERM_BP_5	programmed cell death	34	0.91%
	regulation of protein		
GOTERM_BP_5	kinase activity	27	0.72%
	positive regulation of		
GOTERM_BP_5	programmed cell death	40	1.07%
	negative regulation of		
	cell organization and		
GOTERM_BP_5	biogenesis	14	0.38%
GOTERM_BP_5	regulation of	8	0.21%

	exocytosis		
GOTERM_BP_5	lipid biosynthesis	51	1.37%
	intracellular protein		
GOTERM_BP_5	transport	101	2.71%
	skeletal muscle fiber		
GOTERM_BP_5	development	12	0.32%
	inner ear		
GOTERM_BP_5	morphogenesis	12	0.32%
	positive regulation of		
GOTERM_BP_5	MAPKKK cascade	4	0.11%
	positive regulation of		
GOTERM_BP_5	cellular metabolism	66	1.77%
	embryonic eye		
GOTERM_BP_5	morphogenesis	7	0.19%
	neurotransmitter		
GOTERM_BP_5	catabolism	6	0.16%
	nitrogen compound		
GOTERM_BP_5	biosynthesis	20	0.54%
GOTERM_BP_5	amine biosynthesis	20	0.54%
	salivary gland		
GOTERM_BP_5	morphogenesis	5	0.13%
	negative regulation of		
GOTERM_BP_5	cell growth	8	0.21%
	carbohydrate		
GOTERM_BP_5	biosynthesis	24	0.64%
	regulation of action		
GOTERM_BP_5	potential	9	0.24%
	membrane lipid		
GOTERM_BP_5	metabolism	30	0.80%
GOTERM_BP_5	nucleotide metabolism	50	1.34%
	membrane lipid		
GOTERM_BP_5	biosynthesis	18	0.48%
GOTERM_BP_5	vasoconstriction	7	0.19%
	regulation of striated		
GOTERM_BP_5	muscle development	7	0.19%
	embryonic limb		
GOTERM_BP_5	morphogenesis	16	0.43%
	negative regulation of		
GOTERM_BP_5	cell size	8	0.21%
GOTERM_BP_5	superoxide metabolism	8	0.21%
	interphase of mitotic		
GOTERM_BP_5	cell cycle	15	0.40%
	carboxylic acid		
GOTERM_BP_5	metabolism	100	2.68%
GOTERM_BP_5	blood coagulation	16	0.43%
GOTERM_BP_5	tissue regeneration	4	0.11%
GOTERM_BP_5	small GTPase mediated	62	1.66%

	signal transduction		
	regulation of amino		
GOTERM_BP_5	acid metabolism	13	0.35%
	cytoskeleton		
	organization and		
GOTERM_BP_5	biogenesis	99	2.65%
	photoreceptor cell		
GOTERM_BP_5	development	6	0.16%
	eye photoreceptor cell		
GOTERM_BP_5	differentiation	6	0.16%
	gastrulation (sensu		
GOTERM_BP_5	Deuterostomia)	7	0.19%
	cytokine and		
	chemokine mediated		
GOTERM_BP_5	signaling pathway	12	0.32%
	negative regulation of		
GOTERM_BP_5	protein kinase activity	11	0.29%
	patterning of blood		
GOTERM_BP_5	vessels	8	0.21%
GOTERM_BP_5	bone mineralization	9	0.24%
	regulation of		
	phosphorus		
GOTERM_BP_5	metabolism	14	0.38%
GOTERM_BP_5	regulation of balance	5	0.13%
	integrin-mediated		
GOTERM_BP_5	signaling pathway	23	0.62%
GOTERM_BP_5	amino acid metabolism	52	1.39%
	regulation of peptidyl-		
	tyrosine		
GOTERM_BP_5	phosphorylation	11	0.29%
	peptide hormone		
GOTERM_BP_5	secretion	6	0.16%
	sensory perception of		
GOTERM_BP_5	pain	6	0.16%
	neural crest cell		
GOTERM_BP_5	migration	6	0.16%
	sensory perception of		
GOTERM_BP_5	mechanical stimulus	17	0.46%
GOTERM_BP_5	regulation of secretion	10	0.27%
	regulation of		
GOTERM_BP_5	chemotaxis	4	0.11%
GOTERM_BP_5	positive chemotaxis	4	0.11%
	positive regulation of		
GOTERM_BP_5	protein kinase activity	16	0.43%
GOTERM_BP_5	luteinization	3	0.08%
GOTERM_BP_5	long-term memory	3	0.08%
GOTERM_BP_5	nucleus localization	3	0.08%
GOTERM_BP_5	establishment of	3	0.08%

	nucleus localization		
	norepinephrine		
GOTERM_BP_5	metabolism	3	0.08%
GOTERM_BP_5	endocytosis	37	0.99%

PValue	Genes	List Total	Pop Hits
2.35E-40	Pcdhb16,	2374	150
2.71E-37	Clcn2, Col	12374	707
2.27E-25	C130076O	2374	239
2.13E-22	C130076O	2374	171
2.65E-22	C130076O	2374	151
8.77E-19	C130076O	2374	224
4.75E-18	Cacna1h,	K2374	488
4.39E-16	Rasgrp4,	2374	227
2.91E-13	C130076O	2374	70
4.90E-11	Rasgrp4,	2374	103
5.19E-11	Fzd4, Dkk	2374	100
2.20E-09	Gabrd, Clc	2374	175
1.40E-08	E2f1, Irs2,	2374	111
3.33E-08	Cit, Cd81,	G2374	823
5.81E-08	Cd81, Ras	g2374	105
1.50E-07	Cd81, Ras	g2374	101
1.50E-07	Nr2f1, C13	2374	41
4.48E-07	Vamp2, Nr	x2374	40
6.50E-07	Adcy5, Ad	c2374	13
6.56E-07	Vamp2, Nr	x2374	35
8.24E-07	Slc18a2, S	2374	44
1.07E-06	C130076O	2374	33
2.48E-06	Gadd45b,	l2374	349
1.27E-05	Chat, Gata	2374	11
1.34E-05	Slc38a1, S	2374	70
3.24E-05	Col18a1,	2374	136
5.22E-05	Nat6, Sas	2374	100
1.58E-04	Gadd45b,	C2374	214
1.67E-04	Tnfrsf12a,	2374	11
1.69E-04	Dkk1, Prkc	2374	75
2.76E-04	Tgfb1, Tim	2374	92
2.85E-04	Odc1, Sm	2374	66
6.03E-04	Gadd45b,	C2374	501
6.31E-04	Odc1, Srm	2374	24
7.07E-04	Col18a1,	2374	326
7.74E-04	Nrxn3, Ra	2374	183
7.85E-04	Slc39a5, P	2374	93
8.10E-04	Col18a1,	2374	113
8.31E-04	Slc38a1, S	2374	59
8.31E-04	Ldlr, Fdft1,	2374	59
9.03E-04	C130076O	2374	13

0.001041318	Dkk1, Ppa	p2374	16
0.001063617	Vamp2, S	2374	22
0.001084698	Gata3, Mo	x2374	19
0.001285072	Col18a1,	2374	332
0.001477854	Aldh5a1,	2374	11
0.002415803	Odc1, Srm	2374	52
0.002673927	Pea15, Pr	2374	45
0.003055181	Lrp4, Ncal	d2374	346
0.003132621	Fzd9, Bdn	f2374	15
0.003482629	Vamp2, S	2374	65
0.003538657	Aldoc, Col	12374	275
0.003651994	Pou2f1, C	2374	235
0.003827507	Robo2, Pg	f2374	25
0.004375617	Slc38a1, S	2374	74
0.004375617	Slc38a1, S	2374	74
0.004481767	Nsdhl, Sor	l2374	132
0.00458915	Gucy2f, C	2374	1545
0.005093786	Cd81, Alo	2374	445
0.005644878	Traf7, Tim	p2374	5
0.006089803	Shh, Fgfr1	,2374	37
0.008497994	Chst8, Ba	2374	8
0.01066905	Btg3, Gas1	2374	21
0.010911887	Dmp1, Ru	2374	75
0.011085297	Cd81, Itgb	12374	113
0.011666082	Btg1, Chat	,2374	32
0.012511044	Pgf, Rarb,	S2374	36
0.014367707	Tnfrsf12a,	S2374	6
0.015048096	Lef1, Runx	2374	22
0.01521237	C130076O	2374	33
0.015554708	Mapt, Hda	c2374	12
0.015554708	Dkk1, Wif1	2374	12
0.015637225	Lhx4, Tegt	,2374	120
0.018405333	Gadd45b,	C2374	91
0.018632363	Rarg, Prkc	a2374	148
0.020155367	Mapt, Gsn	,2374	38
0.020989526	Vamp2, S	2374	16
0.02114494	Cd81, Ptd	2374	199
0.021740101	Pex14, Co	p2374	434
0.023865924	Chat, Btg1	,2374	31
0.023865924	Hmx3, Dlx	52374	31
0.023913501	Traf7, Agt,	2374	4
0.024129583	Pou2f1, C	2374	270
0.024287871	Rarg, Mfn	2374	13
0.027246052	Aldh5a1,	2374	10
0.027363142	Otc, Pycrl,	2374	64
0.027363142	Otc, Pycrl,	2374	64
0.028482551	Shh, Fgfr1	,2374	7

0.029919383	Btg1, Mt3,	2374	17
0.031385618	Glce, B4g	2374	82
0.033615993	Kcnmb4,	2374	21
0.034121473	Cd81, Ptd	2374	109
0.034156879	Gucy2c, G	u2374	200
0.034159481	Agpat4, C	2374	57
0.035770527	Kcnmb4,	2374	14
0.035770527	Cenpf, Hd	2374	14
0.036113898	Cyp26b1,	D2374	49
0.041086173	Btg1, Mt3,	2374	18
0.041086173	Mt3, Scd2,	2374	18
0.044027217	Itgb1, Apb	b2374	46
0.046682602	Cd81, Ald	2374	443
0.050258317	Thbd, Anx	a2374	51
0.051316436	Gja1, Plg,	N2374	5
0.051543177	Rasgrp4,	2374	262
0.055276856	Pdgfd, Cd	2374	39
0.059494074	Epb4.1l1,	2374	443
0.061293177	Ntrk2, Nr2	e2374	12
0.061293177	Stat3, Ntrk	22374	12
0.06776281	Ugdh, Lrp	2374	16
0.067865746	Irak1, Stat	32374	36
0.069671077	Gadd45b,	D2374	32
0.070666582	Plxnd1, Pit	x2374	20
0.071463819	Ostn, Pthl	2374	24
0.074228205	Pdgfd, Cd	2374	45
0.074336525	Adcy5, He	x2374	9
0.07664697	A	damts15, 2374	85
0.079373447	Cd81, Gld	2374	221
0.083537506	Cd4, Cd81	2374	33
0.084421493	Trpv4, Gc	2374	13
0.084421493	Penk1, Nd	n2374	13
0.084421493	Pax3, Edn	r2374	13
0.084492514	Accn1, Cd	k2374	59
0.086164537	Traf2, Kcn	m2374	29
0.088265166	Prkca, Sp	2374	6
0.088265166	Prkca, Sp	2374	6
0.089130906	Cd81, Gad	2374	55
0.095628058	Nr5a1, Sta	t2374	3
0.095628058	Ntf5, Chst1	2374	3
0.095628058	Slit1, Ptk2,	2374	3
0.095628058	Slit1, Ptk2,	2374	3
0.095628058	Gata3, Db	h2374	3
0.099964852	Lrp4, Lrp8	2374	153

**Supplementary Table 6. Gene Ontology Analysis (DAVID) of the AGEA dataset.** The AGEA dataset is rich in neuroscientific related genes and generally lacks genes with widespread expression such as those represented by various metabolic, biosynthetic, and basal or homeostatic gene functions.

# Correlation Means

CTX2_3_AUD	103				
AUD	0.9506	0.9375	0.9175	0.8914	
SSp	0.9277	0.9126	0.8977	0.8801	
SSs	0.9333	0.9198	0.9046	0.8867	
VISp	0.9281	0.9265	0.9073	0.8849	
CTX2_3_SSp	427				
AUD	0.9277	0.9158	0.8983	0.8795	
SSp	0.9429	0.9287	0.91	0.8955	
SSs	0.9406	0.9274	0.9091	0.8954	
VISp	0.9268	0.9266	0.9063	0.8814	
CTX2_3_SSs	74				
AUD	0.9333	0.9244	0.9041	0.8823	
SSp	0.9406	0.9315	0.912	0.8971	
SSs	0.9529	0.9419	0.9232	0.9016	
VISp	0.9196	0.9229	0.9034	0.8788	
CTX2_3_VISp	88				
AUD	0.9195	0.9022	0.8853	0.8655	
SSp	0.9182	0.897	0.8804	0.8665	
SSs	0.9112	0.8929	0.8768	0.8681	
VISp	0.945	0.937	0.9128	0.884	
CTX4_AUD	37				
AUD	0.9374	0.9548	0.9427	0.9143	
SSp	0.9156	0.9258	0.9244	0.9072	
SSs	0.9242	0.9362	0.9338	0.9109	
VISp	0.9101	0.931	0.9269	0.9095	
CTX4_SSp	180				
AUD	0.9113	0.926	0.9106	0.885	
SSp	0.9268	0.9444	0.9312	0.9126	
SSs	0.93	0.9442	0.9311	0.9071	
VISp	0.9038	0.9288	0.9196	0.8934	
CTX4_SSs	40				
AUD	0.9174	0.9364	0.9211	0.8948	
SSp	0.9249	0.9439	0.9347	0.9177	
SSs	0.9394	0.957	0.9472	0.9182	
VISp	0.8988	0.925	0.9187	0.8957	
CTX4_VISp	39				
AUD	0.9182	0.923	0.9091	0.8847	
SSp	0.9178	0.9201	0.9088	0.8932	
SSs	0.9139	0.9166	0.9053	0.8907	
VISp	0.9373	0.956	0.9423	0.9119	
CTX5_AUD	112				

AUD	0.9124	0.9388	0.9511	0.945
SSp	0.8947	0.9062	0.9265	0.932
SSs	0.8997	0.9156	0.9338	0.9374
VISp	0.8887	0.9118	0.925	0.9341
CTX5_SSp	394			
AUD	0.8871	0.9181	0.926	0.916
SSp	0.9002	0.923	0.9411	0.9444
SSs	0.9024	0.9267	0.9403	0.935
VISp	0.8776	0.9082	0.9209	0.921
CTX5_SSs	79			
AUD	0.8943	0.9242	0.9331	0.9293
SSp	0.9029	0.9229	0.9403	0.9487
SSs	0.9136	0.9359	0.9532	0.9508
VISp	0.878	0.9061	0.9189	0.9234
CTX5_VISp	76			
AUD	0.8984	0.9205	0.9246	0.9124
SSp	0.8958	0.909	0.9193	0.9189
SSs	0.8936	0.9086	0.9169	0.9142
VISp	0.9094	0.9384	0.9466	0.9401
CTX6a_AUD	68			
AUD	0.885	0.905	0.9318	0.957
SSp	0.8721	0.8763	0.9048	0.9309
SSs	0.8744	0.8834	0.9106	0.945
VISp	0.8667	0.8831	0.9031	0.9362
CTX6a_SSp	313			
AUD	0.8781	0.8975	0.9186	0.9367
SSp	0.8886	0.8965	0.9218	0.9497
SSs	0.8894	0.9001	0.9226	0.9496
VISp	0.8721	0.8905	0.9078	0.9349
CTX6a_SSs	75			
AUD	0.8827	0.902	0.9243	0.9491
SSp	0.8911	0.8973	0.9211	0.9498
SSs	0.8966	0.9063	0.9313	0.964
VISp	0.8722	0.8892	0.9057	0.9316
CTX6a_VISp	47			
AUD	0.8714	0.8926	0.9147	0.9286
SSp	0.8671	0.8749	0.9003	0.9225
SSs	0.8651	0.8763	0.8993	0.9227
VISp	0.8784	0.9011	0.9223	0.9501

#### Correlation Means Norm

CTX2_3_AUD	103			
AUD	1.8453	1.7353	1.5835	1.4334
SSp	1.651	1.5578	1.4707	1.382
SSs	1.6926	1.6049	1.509	1.4119
VISp	1.6501	1.6437	1.5203	1.4021
CTX2_3_SSp	427			
AUD	1.6484	1.5679	1.4667	1.3763



SSp	1.7705	1.6627	1.5347	1.4528
SSs	1.7519	1.6538	1.5292	1.4516
VISp	1.6411	1.6395	1.5106	1.3845
CTX2_3_SSs	74			
AUD	1.6886	1.6216	1.4957	1.3871
SSp	1.7484	1.6817	1.5463	1.4608
SSs	1.8692	1.7726	1.6203	1.4836
VISp	1.5904	1.6109	1.4933	1.3719
CTX2_3_VISp	88			
AUD	1.6055	1.5021	1.4119	1.3213
SSp	1.5969	1.4753	1.3905	1.3276
SSs	1.5514	1.4531	1.3733	1.3334
VISp	1.8233	1.7592	1.5674	1.4047
CTX4_AUD	37			
AUD	1.7203	1.8889	1.7679	1.5613
SSp	1.5646	1.6334	1.6238	1.5163
SSs	1.6213	1.7131	1.6945	1.5366
VISp	1.5344	1.6711	1.6406	1.5298
CTX4_SSp	180			
AUD	1.5422	1.6341	1.537	1.4059
SSp	1.6427	1.7804	1.672	1.5479
SSs	1.6635	1.7788	1.671	1.5152
VISp	1.5002	1.6537	1.5901	1.4447
CTX4_SSs	40			
AUD	1.5805	1.7119	1.5983	1.4478
SSp	1.6267	1.7742	1.6972	1.5777
SSs	1.7381	1.9127	1.8103	1.5802
VISp	1.4703	1.624	1.5811	1.4511
CTX4_VISp	39			
AUD	1.5887	1.624	1.5344	1.4035
SSp	1.5867	1.6045	1.5342	1.447
SSs	1.5619	1.5812	1.5131	1.4326
VISp	1.7376	1.9424	1.7835	1.5524
CTX5_AUD	112			
AUD	1.5464	1.7384	1.8478	1.8041
SSp	1.4485	1.5136	1.6396	1.6831
SSs	1.4757	1.5713	1.694	1.7292
VISp	1.4192	1.5436	1.6257	1.6982
CTX5_SSp	394			
AUD	1.4117	1.5819	1.6334	1.5737
SSp	1.476	1.616	1.7495	1.7886
SSs	1.4883	1.6416	1.743	1.7064
VISp	1.3679	1.5218	1.5975	1.602
CTX5_SSs	79			
AUD	1.4461	1.6243	1.6847	1.665
SSp	1.4891	1.6132	1.7429	1.8294
SSs	1.552	1.713	1.871	1.8619
VISp	1.3681	1.5074	1.5826	1.6149

CTX5_VISp	76				
AUD	1.4695	1.6042	1.635	1.5585	
SSp	1.4569	1.5328	1.5981	1.602	
SSs	1.4457	1.5304	1.5817	1.5683	
VISp	1.5331	1.7509	1.8221	1.7755	
CTX6a_AUD	68				
AUD	1.4	1.5023	1.6766	1.9333	
SSp	1.3439	1.3625	1.502	1.6729	
SSs	1.3537	1.3945	1.5357	1.8007	
VISp	1.3211	1.3919	1.492	1.7118	
CTX6a_SSp	313				
AUD	1.3686	1.4618	1.5837	1.7157	
SSp	1.4172	1.4586	1.6079	1.8472	
SSs	1.4214	1.4775	1.6136	1.8424	
VISp	1.3425	1.4267	1.5183	1.6996	
CTX6a_SSs	75				
AUD	1.3881	1.4855	1.6205	1.8303	
SSp	1.4284	1.4598	1.5999	1.8363	
SSs	1.4559	1.5097	1.673	2.025	
VISp	1.3425	1.4189	1.5044	1.6716	
CTX6a_VISp	47				
AUD	1.3424	1.4407	1.5656	1.6648	
SSp	1.3244	1.3584	1.4814	1.6214	
SSs	1.316	1.3639	1.4753	1.6225	
VISp	1.3724	1.4859	1.6173	1.8688	

#### Correlation SDs

CTX2_3_AUD	103				
AUD	0.0188	0.0166	0.0178	0.0099	
SSp	0.0147	0.0145	0.0142	0.0076	
SSs	0.0128	0.0157	0.0147	0.0067	
VISp	0.0142	0.0088	0.0156	0.0081	
CTX2_3_SSp	427				
AUD	0.0166	0.0125	0.0145	0.0115	
SSp	0.0186	0.017	0.0175	0.0077	
SSs	0.0149	0.0132	0.0109	0.0054	
VISp	0.0139	0.0082	0.016	0.0066	
CTX2_3_SSs	74				
AUD	0.0163	0.0126	0.0165	0.0111	
SSp	0.0174	0.0143	0.0168	0.008	
SSs	0.0198	0.0163	0.0155	0.0078	
VISp	0.015	0.0079	0.0164	0.0068	
CTX2_3_VISp	88				
AUD	0.0131	0.0139	0.0139	0.005	
SSp	0.014	0.016	0.0155	0.0057	
SSs	0.0124	0.0131	0.0097	0.0034	
VISp	0.0179	0.0142	0.0199	0.0114	
CTX4_AUD	37				

AUD	0.0229	0.0175	0.0177	0.0103
SSp	0.0149	0.0116	0.0117	0.0072
SSs	0.0118	0.0096	0.0149	0.007
VISp	0.0191	0.0073	0.0126	0.009
CTX4_SSp	180			
AUD	0.0236	0.0136	0.0167	0.0139
SSp	0.0221	0.0162	0.0191	0.0093
SSs	0.0193	0.0112	0.0142	0.0081
VISp	0.021	0.0061	0.0156	0.0078
CTX4_SSs	40			
AUD	0.0235	0.0129	0.0173	0.0129
SSp	0.0208	0.012	0.0152	0.0089
SSs	0.0219	0.0166	0.0175	0.0098
VISp	0.021	0.0064	0.0143	0.0077
CTX4_VISp	39			
AUD	0.0167	0.0107	0.0127	0.0058
SSp	0.0125	0.01	0.0129	0.0053
SSs	0.0098	0.007	0.0105	0.0036
VISp	0.0209	0.014	0.0205	0.0131
CTX5_AUD	112			
AUD	0.021	0.017	0.0179	0.0123
SSp	0.0136	0.0161	0.0164	0.0076
SSs	0.0093	0.0088	0.0116	0.0074
VISp	0.0175	0.0079	0.0122	0.0089
CTX5_SSp	394			
AUD	0.023	0.015	0.0142	0.0141
SSp	0.0191	0.0166	0.0166	0.0104
SSs	0.0182	0.0124	0.0112	0.0079
VISp	0.0202	0.009	0.0105	0.0072
CTX5_SSs	79			
AUD	0.0215	0.0133	0.0132	0.014
SSp	0.0171	0.0133	0.0123	0.0088
SSs	0.0188	0.015	0.0156	0.0091
VISp	0.019	0.0082	0.01	0.0075
CTX5_VISp	76			
AUD	0.0185	0.012	0.0108	0.0052
SSp	0.0132	0.0126	0.0116	0.0057
SSs	0.0106	0.006	0.0076	0.0043
VISp	0.0214	0.0139	0.0178	0.0147
CTX6a_AUD	68			
AUD	0.0161	0.0138	0.0226	0.0159
SSp	0.012	0.0176	0.0236	0.0095
SSs	0.0069	0.0087	0.0176	0.009
VISp	0.0138	0.0063	0.0189	0.0119
CTX6a_SSp	313			
AUD	0.0154	0.0102	0.0185	0.0161
SSp	0.0138	0.0155	0.0199	0.0096
SSs	0.0109	0.01	0.0175	0.006

VISp	0.0145	0.0059	0.0158	0.011
CTX6a_SSs	75			
AUD	0.0151	0.0099	0.0182	0.016
SSp	0.0128	0.0145	0.0178	0.0086
SSs	0.0126	0.0117	0.0201	0.0087
VISp	0.014	0.0055	0.0148	0.0097
CTX6a_VISp	47			
AUD	0.0144	0.0124	0.0184	0.0043
SSp	0.0117	0.0167	0.0194	0.0058
SSs	0.0069	0.007	0.0144	0.0047
VISp	0.0176	0.0125	0.0231	0.0188

# **Correlation SDs Norm**

CTX2_3_AUD	103			
AUD	0.3211	0.1823	0.133	0.0496
SSp	0.107	0.0955	0.0788	0.0359
SSs	0.1034	0.1197	0.092	0.032
VISp	0.0961	0.0659	0.0912	0.0382
CTX2_3_SSp	427			
AUD	0.1193	0.0847	0.0824	0.0504
SSp	0.2212	0.1493	0.1171	0.0408
SSs	0.1375	0.1063	0.0687	0.0278
VISp	0.0896	0.0586	0.0886	0.0298
CTX2_3_SSs	74			
AUD	0.1268	0.0961	0.1022	0.0491
SSp	0.1555	0.1185	0.1114	0.0421
SSs	0.4116	0.1799	0.1201	0.0432
VISp	0.089	0.0526	0.0889	0.0299
CTX2_3_VISp	88			
AUD	0.0889	0.0869	0.0733	0.0209
SSp	0.0867	0.0873	0.0773	0.0235
SSs	0.0743	0.0719	0.0465	0.0138
VISp	0.2674	0.16	0.1389	0.0552
CTX4_AUD	37			
AUD	0.2198	0.4077	0.1996	0.0649
SSp	0.0898	0.0871	0.0827	0.0428
SSs	0.0821	0.0852	0.1249	0.0437
VISp	0.1089	0.0577	0.0935	0.0537
CTX4_SSp	180			
AUD	0.1361	0.0959	0.103	0.0634
SSp	0.1724	0.243	0.1749	0.0578
SSs	0.1426	0.118	0.1138	0.0469
VISp	0.1098	0.0433	0.0958	0.0389
CTX4_SSs	40			
AUD	0.1506	0.1102	0.1307	0.0629
SSp	0.1445	0.1268	0.1351	0.0599
SSs	0.21	0.331	0.2056	0.0661
VISp	0.1052	0.0438	0.089	0.0388

CTX4_VISp	39				
AUD	0.1011	0.0789	0.0814	0.0275	
SSp	0.0754	0.0673	0.0793	0.0267	
SSs	0.0582	0.0454	0.0617	0.0184	
VISp	0.2083	0.3897	0.231	0.0827	
CTX5_AUD	112				
AUD	0.1323	0.1735	0.287	0.1359	
SSp	0.0687	0.096	0.124	0.0643	
SSs	0.0503	0.0589	0.0994	0.069	
VISp	0.0822	0.0488	0.0903	0.0753	
CTX5_SSp	394				
AUD	0.1061	0.0945	0.1018	0.088	
SSp	0.1049	0.1308	0.1964	0.1132	
SSs	0.099	0.0968	0.1073	0.0673	
VISp	0.0876	0.0525	0.0699	0.0492	
CTX5_SSs	79				
AUD	0.106	0.0918	0.1094	0.0988	
SSp	0.0915	0.095	0.1164	0.0995	
SSs	0.1195	0.1497	0.287	0.1208	
VISp	0.0816	0.0462	0.0661	0.0515	
CTX5_VISp	76				
AUD	0.0926	0.0825	0.0827	0.0326	
SSp	0.0665	0.0749	0.0778	0.0383	
SSs	0.0525	0.0353	0.0499	0.0283	
VISp	0.1354	0.1561	0.265	0.1651	
CTX6a_AUD	68				

**Supplementary Table 7. Correlation means and standard deviations for the cortex example in Figure 6f.** The layer and area domain is indicated together with the number of voxels in that domain. Data are given as raw correlation and Fischer rho-to-z transformed normal variates.

## **Links**

All Allen Brain Atlas image data, Allen Reference Atlas plates, AGEA 3D volumes and associated meta-data are available for free public access at <http://mouse.brain-map.org>. Specific URLs for the manuscript figures are provided below.

**Figure 1a ARA plate:** <http://mouse.brain-map.org/viewImage.do?imageId=130958>

**Figure 1c Tac2 ISH:** <http://mouse.brain-map.org/brain/Tac2/77279001/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=77284606>

**Figure 1c Tac2 expression:** <http://mouse.brain-map.org:80/viewImage.do?imageId=77284606&coordSystem=pixel&x=6141.17613817732&y=4747.27552589181&z=29.4576664997496&initExp=y>

**Figure 1e AGEA correlation (seed):** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=5200,3175,2425&mapPoint=5200,3175,2425&lowerRange=0.5&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=5200,3175,2425&mapPoint=5200,3175,2425&lowerRange=0.5&upperRange=1)

**Figure 1e AGEA correlation (green target):** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=5200,2552,3367&mapPoint=5200,2552,3367&lowerRange=0.5&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=5200,2552,3367&mapPoint=5200,2552,3367&lowerRange=0.5&upperRange=1)

**Figure 1e AGEA correlation (blue target):** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=5200,4488,3323&mapPoint=5200,4488,3323&lowerRange=0.5&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=5200,4488,3323&mapPoint=5200,4488,3323&lowerRange=0.5&upperRange=1)

**Figure 1h AGEA correlation (seed):** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=5200,3175,2425&mapPoint=5200,3175,2425&lowerRange=0.5&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=5200,3175,2425&mapPoint=5200,3175,2425&lowerRange=0.5&upperRange=1)

**Figure 2a AGEA correlation:** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=7180,4000,4000&mapPoint=7180,4000,4000&lowerRange=0.7&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=7180,4000,4000&mapPoint=7180,4000,4000&lowerRange=0.7&upperRange=1)

**Figure 2b ARA Level 73:** <http://mouse.brain-map.org:80/viewImage.do?imageId=130938&coordSystem=pixel&x=2918.34765625&y=1931.16796875&z=29.893743775464>

**Figure 2c LOC433228:** <http://mouse.brain-map.org/brain/LOC433228/73788454/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=73769595>

**Figure 2d Kcnab3:** <http://mouse.brain-map.org/brain/Kcnab3/73817925/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=73813883>

**Figure 3a AGEA correlation:** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=7600,4400,5400&mapPoint=7600,4400,5400&lowerRange=0.80&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=7600,4400,5400&mapPoint=7600,4400,5400&lowerRange=0.80&upperRange=1)

**Figure 3b ARA Level 77:** <http://mouse.brain-map.org:80/viewImage.do?imageId=130934&coordSystem=pixel&x=2889.453125&y=2075.640625&z=27.6544137618832>

**Figure 3c Ddc8:** <http://mouse.brain-map.org/brain/Ddc8/73615805/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=73531450>

**Figure 3d Rprm:** <http://mouse.brain-map.org/brain/Rprm/71836875/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=71713391>

**Figure 4a AGEA Correlation:** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=4625,4010,7125&mapPoint=4625,4010,7125&lowerRange=0.5938&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=4625,4010,7125&mapPoint=4625,4010,7125&lowerRange=0.5938&upperRange=1)

**Figure 4b AGEA Clusters (Depth=0):** [http://mouse.brain-map.org/agea/all\\_coronal?clusters&seedPoint=4625,4010,7125&mapPoint=4625,4010,7125&treeLevel=0](http://mouse.brain-map.org/agea/all_coronal?clusters&seedPoint=4625,4010,7125&mapPoint=4625,4010,7125&treeLevel=0)

**Figure 4c AGEA Clusters (Depth=4):** [http://mouse.brain-map.org/agea/all\\_coronal?clusters&seedPoint=4625,4010,7125&mapPoint=4625,4010,7125&treeLevel=4](http://mouse.brain-map.org/agea/all_coronal?clusters&seedPoint=4625,4010,7125&mapPoint=4625,4010,7125&treeLevel=4)

**Figure 5a BC053994:** <http://mouse.brain-map.org/brain/BC053994/77340462/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=77345774>

**Figure 5b Ddit41:** <http://mouse.brain-map.org/aba/mouse/brain/Ddit41/71836878/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=71726386>

**Figure 5c Ace:** <http://mouse.brain-map.org/aba/mouse/brain/Ace/73512499/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=73268040>

**Figure 5d Wfs1:** <http://mouse.brain-map.org/aba/mouse/brain/Wfs1/74881161/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=74825043>

**Figure 5e Btg1:** <http://mouse.brain-map.org/aba/mouse/brain/Btg1/73718576/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=73700498>

**Figure 5f Npy1r:** <http://mouse.brain-map.org/aba/mouse/brain/Npy1r/72103807/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=71960345>

**Figure 5g mCG145872:** <http://mouse.brain-map.org/brain/mCG145872/74512028/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=70967221>

**Figure 5h Thbs3:** <http://mouse.brain-map.org/brain/Thbs3/74657923/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=69847012>

**Figure 5i AGEA Clusters (coronal):** [http://mouse.brain-map.org/agea/all\\_coronal?clusters&seedPoint=4625,4010,7125&mapPoint=4625,4010,7125&treeLevel=4](http://mouse.brain-map.org/agea/all_coronal?clusters&seedPoint=4625,4010,7125&mapPoint=4625,4010,7125&treeLevel=4)

**Figure 5i AGEA Clusters (sagittal):** [http://mouse.brain-map.org/agea/all\\_coronal?clusters&seedPoint=4625,4010,7125&mapPoint=5878,4010,2816&treeLevel=4](http://mouse.brain-map.org/agea/all_coronal?clusters&seedPoint=4625,4010,7125&mapPoint=5878,4010,2816&treeLevel=4)

*Links for supplementary data*

**Supplementary Figure 1:** <http://mouse.brain-map.org/atlas/coronal/CTX.html?level=67>  
<http://mouse.brain-map.org/viewImage.do?imageId=130944>

**Supplementary Figure 2a:** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=4825,2875,8475&mapPoint=4800,2800,8375&lowerRange=0.5&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=4825,2875,8475&mapPoint=4800,2800,8375&lowerRange=0.5&upperRange=1)

**Supplementary Figure 2b:** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=4825,2875,8475&mapPoint=4800,2800,8375&lowerRange=0.85&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=4825,2875,8475&mapPoint=4800,2800,8375&lowerRange=0.85&upperRange=1)

**Supplementary Figure 2c:** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=4825,2875,8475&mapPoint=4800,2800,8375&lowerRange=0.92&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=4825,2875,8475&mapPoint=4800,2800,8375&lowerRange=0.92&upperRange=1)

**Supplementary Figure 3a:** [http://mouse.brain-map.org/agea/all\\_coronal?clusters&seedPoint=6600,4000,5675&mapPoint=6600,4000,5675&treeLevel=0](http://mouse.brain-map.org/agea/all_coronal?clusters&seedPoint=6600,4000,5675&mapPoint=6600,4000,5675&treeLevel=0)

**Supplementary Figure 3b:** [http://mouse.brain-map.org/agea/all\\_coronal?clusters&seedPoint=6600,4000,5675&mapPoint=6600,4000,5675&treeLevel=7](http://mouse.brain-map.org/agea/all_coronal?clusters&seedPoint=6600,4000,5675&mapPoint=6600,4000,5675&treeLevel=7)

**Supplementary Figure 4a:** [http://mouse.brain-map.org/agea/all\\_coronal?geneFinder&seedPoint=7600,4200,6000](http://mouse.brain-map.org/agea/all_coronal?geneFinder&seedPoint=7600,4200,6000)

**Supplementary Figure 4b:** <http://mouse.brain-map.org/agea/GeneFinder.html?seedPoint=7600,4200,6000>

**Supplementary Figure 5a, Layer 1, A930038C07Rik:** <http://mouse.brain-map.org:80/viewImage.do?imageId=71898421&coordSystem=pixel&x=4964.43924120769&y=3936.91159729596&z=11.7531391212383>

**Supplementary Figure 5b, Layer 2, 9830123M21Rik:** <http://mouse.brain-map.org:80/viewImage.do?imageId=75949172&coordSystem=pixel&x=4938.02434667058&y=3750.00771636432&z=12.2835413186597>



**Supplementary Figure 5c, Layer 2/3, *Rasgrf2*:** <http://mouse.brain-map.org:80/viewImage.do?imageId=73959358&coordSystem=pixel&x=4959.49658370288&y=3844.36959002774&z=12.7590343818581>

**Supplementary Figure 5d, Layer 3/4, *LOC433228*:** <http://mouse.brain-map.org:80/viewImage.do?imageId=73770201&coordSystem=pixel&x=5280.11898648389&y=4444.59800845602&z=11.5110436432638>

**Supplementary Figure 5e, Layer 5, *Serpine2*:** <http://mouse.brain-map.org:80/viewImage.do?imageId=73995717&coordSystem=pixel&x=4919.11137953908&y=4062.11692687822&z=12.7590551181102>

**Supplementary Figure 5f, Layer 5 (deep), *C030003D03Rik*:** <http://mouse.brain-map.org:80/viewImage.do?imageId=79604127&coordSystem=pixel&x=5055.84227035817&y=3917.74003142121&z=12.652097867741>

**Supplementary Figure 5g, Layer 6, *Cdh24*:** <http://mouse.brain-map.org:80/viewImage.do?imageId=69908198&coordSystem=pixel&x=5364.11481054433&y=4065.90072347936&z=12.7725709943964>

**Supplementary Figure 5h, Layer 6b, *Cplx3*:** <http://mouse.brain-map.org:80/viewImage.do?imageId=70828722&coordSystem=pixel&x=5657.7534583421&y=4452.61951681185&z=11.318553092182>

**Supplementary Figure 6a *Cplx3*:** <http://mouse.brain-map.org/viewImage.do?imageId=70828718>

**Supplementary Figure 6b *Ctgf*:** <http://mouse.brain-map.org/viewImage.do?imageId=79560438>

**Supplementary Figure 6c *Tle1*:** <http://mouse.brain-map.org/viewImage.do?imageId=69501>

**Supplementary Figure 6d *Cdh24*:** <http://mouse.brain-map.org/viewImage.do?imageId=69908198>

**Supplementary Figure 6e *Tpbp*:** <http://mouse.brain-map.org/viewImage.do?imageId=76060789>

**Supplementary Figure 6f *Gng12*:** <http://mouse.brain-map.org/viewImage.do?imageId=71897015>

**Supplementary Figure 6g *Rprm*:** <http://mouse.brain-map.org/viewImage.do?imageId=71713403>

**Supplementary Figure 6h *Tle4*:** <http://mouse.brain-map.org/viewImage.do?imageId=73451046>

**Supplementary Figure 7a:** <http://mouse.brain-map.org/viewImage.do?imageId=130937>

**Supplementary Figure 7b:** <http://mouse.brain-map.org/viewImage.do?imageId=130925>

**Supplementary Figure 9b:** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=4000,3625,6425&mapPoint=4000,3625,6425&lowerRange=0.438&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=4000,3625,6425&mapPoint=4000,3625,6425&lowerRange=0.438&upperRange=1)

**Supplementary Figure 9c:** [http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=4000,3625,6425&mapPoint=4000,3625,6425&lowerRange=0.8013&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=4000,3625,6425&mapPoint=4000,3625,6425&lowerRange=0.8013&upperRange=1)

**Supplementary Figure 9d *Tnfrsf19* (sagittal):** <http://mouse.brain-map.org/brain/Tnfrsf19/75692878/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=75569659>

**Supplementary Figure 9d *Tnfrsf19* (coronal):** <http://mouse.brain-map.org/brain/Tnfrsf19/74425524/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=74352564>

**Supplementary Figure 9d *LOC277860*:** <http://mouse.brain-map.org/brain/LOC277860/74581425/thumbnails.html>  
<http://mouse.brain-map.org/viewImage.do?imageId=74478306>

**Supplementary Figure 10:** <http://mouse.brain-map.org/viewImage.do?imageId=70400133>  
<http://mouse.brain-map.org/viewImage.do?imageId=73733958>  
[http://mouse.brain-map.org/agea/all\\_coronal?correlation&seedPoint=3400,4800,6600&mapPoint=3400,4800,6600&lowerRange=0.5313&upperRange=1](http://mouse.brain-map.org/agea/all_coronal?correlation&seedPoint=3400,4800,6600&mapPoint=3400,4800,6600&lowerRange=0.5313&upperRange=1)  
<http://mouse.brain-map.org/agea/GeneFinder.html?seedPoint=3400,4800,6600>

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